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(54) Title: VIRULENCE GENES, PROTEINS, AND THEIR USE

(57) Abstract: A series of genes from *Pseudomonas aeruginosa* and *Klebsiella* are shown to encode products that are implicated in virulence. The identification of these genes therefore allows attenuated microorganisms to be produced. Furthermore, the genes or their encoded products can be used to identify antimicrobial drugs, diagnostic methods for the identification of a pathogen-associated disease, and in the manufacture of vaccines.

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VIRULENCE GENES, PROTEINS, AND THEIR USE

FIELD OF THE INVENTION

This invention relates to virulence genes and proteins, and their use. More particularly, it relates to genes and proteins/peptides obtained from gram-negative bacteria, and their use in therapy and in screening for drugs.

BACKGROUND OF THE INVENTION

According to health care experts, infectious diseases caused by microbes are responsible for more deaths worldwide than any other single cause. The current estimate of the annual cost of medical care for treating infectious diseases in the United States alone is about \$120 billion. While antibiotic treatment is effective for many microbial infections, antibiotic resistance among pathogenic bacteria is a growing health concern. Indeed, the American Medical Association has concluded that, "the global increase in resistance to antimicrobial drugs, including the emergence of bacterial strains that are resistant to all available antibacterial agents, has created a public health problem of potentially crisis proportions."

Pseudomonas and *Klebsiella* are two genres of gram-negative bacteria that pose a significant health risk to infected host organisms, in part, due to their resistance to many antibiotics. These bacteria are noted for causing life-threatening infections, particularly in the lung. Cancer and burn patients also commonly suffer serious *Pseudomonas* infections, as do certain other individuals with immune system deficiencies. While *Klebsiella* sp. is responsible for many types of infections, outside of a medical setting, the most common infection caused by *Klebsiella* bacteria is pneumonia.

There is a need in the art for new antimicrobial therapeutic strategies.

SUMMARY OF THE INVENTION

The present invention is based, in part, on the discovery of 46 genes, when mutated lower the virulence of a gram-negative bacterium, and can be used in new antimicrobial therapeutic strategies. The invention provides attenuated bacterial mutants that are derived from pathogenic strains. These attenuated bacterial stains have a mutation in a VIRX gene identified herein as VIR1, VIR2, VIR3, VIR4, VIR5, VIR6, VIR7, VIR8, VIR9, VIR10, VIR11, VIR12, VIR13, VIR14, VIR15, VIR16, VIR17, VIR18, VIR19, VIR20, VIR21, VIR22, VIR23, VIR24, VIR25, VIR26, VIR27, VIR28, VIR29, VIR30, VIR31, VIR32, VIR33, VIR34, VIR35, VIR36, VIR37, VIR38, VIR39, VIR40, VIR41, VIR42, VIR43, VIR44, VIR45, and VIR46; and show reduced inhibition of *Dictyostelium* amoeba growth when compared to the growth observed in the presence of an isogenic bacterial strain. The term, "pathogenic," as used herein, is defined as an agent's ability to cause disease, damage or harm to a host organism. The term, "attenuated," as used herein, means an organism made less virulent relative to an isogenic pathogenic organism. The term, "mutant," as used herein, an organism carrying a specific mutation of a gene that is expressed in the organism's phenotype. A mutation may be insertional inactivation or deletion of a gene. It is preferred that the mutation be an insertional inactivation of a gene.

The invention also provides attenuated bacterial mutants that are derived from pathogenic gram-negative bacterial strains. These attenuated gram-negative bacterial strains have a mutation in a VIRX gene identified herein as VIR1, VIR2, VIR3, VIR4, VIR5, VIR6, VIR7, VIR8, VIR9, VIR10, VIR11, VIR12, VIR13, VIR14, VIR15, VIR16, VIR17, VIR18, VIR19, VIR20, VIR21, VIR22, VIR23, VIR24, VIR25, VIR26, VIR27, VIR28, VIR29, VIR30, VIR31, VIR32, VIR33, VIR34, VIR35, VIR36, VIR37, VIR38, VIR39, VIR40, VIR41, VIR42, VIR43, VIR44, VIR45, and VIR46; and show reduced inhibition of *Dictyostelium* amoeba growth when compared to the growth observed in the presence of an isogenic bacterial strain. A mutation may be insertional inactivation or deletion of a gene. It is preferred that the mutation be an insertional inactivation of a gene. It is also preferred that the attenuated gram-negative bacterial mutant be derived from a *Pseudomonas* or *Klebsiella* spp. It is more preferred that the attenuated gram-negative bacterial mutant is a strain of *P. aeruginosa* or *K. pneumoniae*.

The invention additionally provides for a VIRX gene that may be part of an operon. The term, "operon," as used herein, is a unit of bacterial gene expression and regulation

comprising several genes, usually with complementary functions. Insertion in a gene in an operon typically interferes with the function of this gene and of other genes located downstream or upstream in the operon. The function attributed to a gene refers to its function and/or that of any gene located downstream or upstream in the same operon. Accordingly, the invention also provides for a bacterial strain comprising an operon encoding a gene selected from the group consisting of VIR1, VIR2, VIR3, VIR4, VIR5, VIR6, VIR7, VIR8, VIR9, VIR10, VIR11, VIR12, VIR13, VIR14, VIR15, VIR16, VIR17, VIR18, VIR19, VIR20, VIR21, VIR22, VIR23, VIR24, VIR25, VIR26, VIR27, VIR28, VIR29, VIR30, VIR31, VIR32, VIR33, VIR34, VIR35, VIR36, VIR37, VIR38, VIR39, VIR40, VIR41, VIR42, VIR44, VIR45, and VIR46, wherein the bacterial strain includes a mutation that reduces expression of the VIRX gene relative to an isogenic bacterial strain lacking the mutation. In one embodiment, the the mutation reduces inhibition of *Dictyostelium* amoeba growth when compared to the growth of *Dictyostelium* amoeba in the presence of an isogenic bacterial strain lacking the mutation.

The invention provides for one or more of the following attenuated *Pseudomonas* mutant strains: MUT1; MUT2; MUT3; MUT4; MUT5; MUT6; MUT7; MUT8; MUT9; MUT10; MUT11; MUT12; MUT13; MUT14; MUT15; MUT16; MUT17; MUT18; and MUT19. The invention also provides for one or more of the following attenuated *Klebsiella* mutant strains: MUT20; MUT21; MUT22; MUT23; MUT24; MUT25; MUT26; MUT27; MUT28; MUT29; MUT30; MUT31; MUT32; MUT33; MUT34; MUT35; MUT36; MUT37; MUT38; MUT39; MUT40; MUT41; MUT42; MUT43; MUT44; MUT45; and MUT46.

The invention additionally provides a method for identifying an antimicrobial drug, wherein a candidate composition is contacted with at least one polypeptide encoded by a gene selected from the group consisting of VIR1, VIR2, VIR3, VIR4, VIR5, VIR6, VIR7, VIR8, VIR9, VIR10, VIR11, VIR12, VIR13, VIR14, VIR15, VIR16, VIR17, VIR18, VIR19, VIR20, VIR21, VIR22, VIR23, VIR24, VIR25, VIR26, VIR27, VIR28, VIR29, VIR30, VIR31, VIR32, VIR33, VIR34, VIR35, VIR36, VIR37, VIR38, VIR39, VIR40, VIR41, VIR42, VIR43, VIR44, VIR45 and VIR46. The biological activity of polypeptide in the presence of the candidate composition is compared with the biological activity of the polypeptide in the absence of the candidate composition. Alteration of the biological activity of the polypeptide indicates that the candidate composition is an antimicrobial drug. In some embodiments, the candidate composition contains at least two molecules. The candidate

composition can contain at least one molecule less than about 500 Daltons or at least one molecule greater than about 500 Daltons. The candidate composition can be, *e.g.*, an immunoglobulin, polysaccharide, lipid, nucleic acid, or combination thereof.

The invention additionally provides a method for identifying an antimicrobial drug, wherein a candidate composition is contacted with at least one polynucleotide encoded by a gene selected from the group consisting of VIR1, VIR2, VIR3, VIR4, VIR5, VIR6, VIR7, VIR8, VIR9, VIR10, VIR11, VIR12, VIR13, VIR14, VIR15, VIR16, VIR17, VIR18, VIR19, VIR20, VIR21, VIR22, VIR23, VIR24, VIR25, VIR26, VIR27, VIR28, VIR29, VIR30, VIR31, VIR32, VIR33, VIR34, VIR35, VIR36, VIR37, VIR38, VIR39, VIR40, VIR41, VIR42, VIR43, VIR44, VIR45, and VIR46. The expression of the polynucleotide in the presence of the candidate composition is compared with the expression of the polynucleotide in the absence of the candidate composition. Alteration of the expression of the polynucleotide indicates that the candidate composition is an antimicrobial drug. In some embodiments, the candidate composition contains at least two molecules. The candidate composition can contain at least one molecule less than about 500 Daltons or at least one molecule greater than about 500 Daltons. The candidate composition can be a polypeptide, polysaccharide, lipid, nucleic acid, *e.g.*, ribonucleic acid, or combination thereof. In a preferred embodiment, the ribonucleic acid of the candidate composition is a small interfering ribonucleic acid.

The invention additionally provides a method for determining the degree of virulence of a pathogen present in a subject, comprising:

(a) measuring the level of expression of at least one polypeptide encoded by a gene selected from the group consisting of VIR1, VIR2, VIR3, VIR4, VIR5, VIR6, VIR7, VIR8, VIR9, VIR10, VIR11, VIR12, VIR13, VIR14, VIR15, VIR16, VIR17, VIR18, VIR19, VIR20, VIR21, VIR22, VIR23, VIR24, VIR25, VIR26, VIR27, VIR28, VIR29, VIR30, VIR31, VIR32, VIR33, VIR34, VIR35, VIR36, VIR37, VIR38, VIR39, VIR40, VIR41, VIR42, VIR43, VIR44, VIR45, and VIR46, in a sample from the first subject; and

(b) comparing the amount of the polypeptide in the sample of step (a) to the amount of the polypeptide present in a control sample from a second subject known not to have the presence of the pathogen, wherein an alteration in the

expression level of the polypeptide in the first subject as compared to the control sample indicates the degree of virulence of the pathogen.

In a preferred embodiment, the subject is a mammal. It is more preferred that the subject is a human.

5 The invention also provides a method for determining the degree of virulence of a pathogen present in a subject, comprising:

(a) measuring the level of expression of at least one polynucleotide encoded by a gene selected from the group consisting of VIR1, VIR2, VIR3, VIR4, VIR5, VIR6, VIR7, VIR8, VIR9, VIR10, VIR11, VIR12, VIR13, VIR14, VIR15, VIR16, VIR17, VIR18, VIR19, 10 VIR20, VIR21, VIR22, VIR23, VIR24, VIR25, VIR26, VIR27, VIR28, VIR29, VIR30, VIR31, VIR32, VIR33, VIR34, VIR35, VIR36, VIR37, VIR38, VIR39, VIR40, VIR41, VIR42, VIR44, VIR45, and VIR46, in a sample from the first subject; and

(b) comparing the amount of the polynucleotide in the sample of step (a) to the amount of the polynucleotide present in a control sample from a second subject known not to 15 have the presence of the pathogen, wherein an alteration in the expression level of the polypeptide in the first subject as compared to the control sample indicates the degree of virulence of the pathogen.

In a preferred embodiment, the subject is a mammal. It is more preferred that the subject is a human.

20 The invention additionally provides attenuated bacterial strains that can be used as vaccines and as vectors for foreign antigens and for foreign DNA. These attenuated bacterial strains are useful for the preparation of vaccines effective against diseases associated with the corresponding bacterial strains. In a preferred embodiment, the attenuated bacterial strains are derived from *Pseudomonas* or *Klebsiella* spp.

25 The invention additionally provides attenuated bacterial strains that can be used as vectors for foreign genes cloned from other pathogens that will be expressed into proteins, and will raise protective immune responses against the pathogens from which they are derived. In a preferred embodiment, the attenuated bacterial strains used as the vectors are derived from *Pseudomonas* or *Klebsiella* spp.

Unless otherwise defined, all technical and scientific terms used herein have the same meaning as commonly understood by one of ordinary skill in the art to which this invention belongs. Although methods and materials similar or equivalent to those described herein can be used in the practice or testing of the invention, suitable methods and materials are described below. All publications, patent applications, patents, and other references mentioned herein are incorporated by reference in their entirety. In the case of conflict, the present specification, including definitions, will control. In addition, the materials, methods, and examples are illustrative only and not intended to be limiting.

Other features and advantages of the invention will be apparent from the following detailed description and claims.

DETAILED DESCRIPTION OF THE INVENTION

The present invention is based, in part, on the discovery of 46 genes when mutated lower the virulence of a gram-negative bacterium. Nineteen of these virulence genes were identified in *P. aeruginosa* PT894, while the remaining 27 genes were derived from mutagenesis of *Klebsiella*. These bacterial mutants have attenuated virulence relative to isogenic bacterial strains and are designated "MUTX." Provided herein are virulence genes affected in each novel, attenuated MUTX strain, as well as the nucleotides and polypeptides encoded thereby. The sequences encoded by the affected genes are collectively referred to as "VIRX nucleic acids" or "VIRX polynucleotides" and the corresponding encoded polypeptides are referred to as "VIRX polypeptides" or "VIRX proteins." Unless indicated otherwise, "VIRX" is meant to refer to any of the novel sequences disclosed herein.

The peptides and genes of the invention are useful for the preparation of therapeutic agents to treat infection because they attenuate the virulence of the wild-type pathogen. Therapy can be preventative or therapeutic. A subject receiving therapy can be, *e.g.*, a human, a non-human primate (such as an ape, gorilla, or chimpanzee), cow, horse, pig, sheep, dog, cat, or rodent (including mouse or rat).

I. IDENTIFICATION OF *PSEUDOMONAS* AND *KLEBSIELLA* GENES ENCODING VIRULENCE FACTORS

Genes encoding virulence factors (*e.g.*, pathogens or toxins) to a host organism were

identified by comparing the growth of *Dictyostelium discoideum*, in the presence and absence of test mutants of *Pseudomonas* and *Klebsiella* with an identifiable genetic alteration as detailed in International Application PCT/IB02/03277, filed June 7, 2002. *Dictyostelium* amoebae feed phagocytically upon bacteria such as *K. pneumoniae*. When *Dictyostelium* cells are plated with *K. pneumoniae* bacteria, each amoeba creates a plaque in the bacterial lawn in the region where bacteria have been phagocytosed. Addition of pathogenic bacteria, e.g., *P. aeruginosa* strain PT894 to the lawn of *K. pneumoniae* bacteria, inhibits the growth of the amoebae.

Pseudomonas test mutants were made by transposon insertion according to known methods in the art and tested for virulence in a *Dictyostelium* growth assay (see, PCT/IB02/03277, filed June 7, 2002). *Klebsiella* mutants were also made by transposon insertion according to known methods in the art and tested for virulence in a *Dictyostelium* growth assay (see, PCT/IB02/03277, filed June 7, 2002) using the *PHG1a* mutant *Dictyostelium* strain (Cornillon *et al.*, J. Biol. Chem., 275(44): 34287-92, 2000), a strain which was found to be particularly sensitive to virulent bacteria. Specifically, the *Klebsiella* mutants were obtained by standard bacteria electroporation technique using the plasposon pNKBOR (Genbank accession number: AF310136) and selected on solid LB medium containing 50 µg/ml kanamycin (Rossignol *et al.*, Res. Microbiol., 152(5): 481-5, 2001). Other mutagenesis methods known in the art, e.g., ultraviolet radiation exposure, treatment with intercalating agent or transducing phage, may also be used to generate mutants. Mutations yielding reduced virulence were identified where the growth of the *Dictyostelium* test host organism exposed to the mutant pathogen was greater than the *Dictyostelium* test host organism exposed to wild-type pathogen. Specific genetic mutations in pathogens displaying reduced virulence were subsequently identified and characterized by techniques well known in the art. Identification of specific gene mutations in *Klebsiella* mutants was performed by plasmid rescue and cloning of the genomic DNA at the insertion site mutant using the BglII or ApaI restriction enzyme according to (Rossignol *et al.*, Res. Microbiol., 152(5): 481-5, 2001). Identification of specific gene mutations in *Pseudomonas* mutants was performed by subcloning the transposon and surrounding bacteria genomic DNA into an acceptor plamid. DNA sequencing was performed on amplified rescued plasmids, in order to identify the insertion site of the transposon. Rat mortality assays such as that described by Join-Lambert *et al.*, Antimicrob. Agents Chemother., 45(2): 571-6, 2001, can be used to

corroborate attenuated virulence activity in a mammalian host.

The 19 *Pseudomonas* attenuated MUTX organisms harboring the VIRX genes are summarized below in Table 1.

Table 1

STRAIN	AFFECTED VIRULENCE GENE(S)	REFERENCE
MUT1	anthranilate phosphoribosyltransferase (trpD; PA0650)	Essar <i>et al.</i> , J. Bacteriol., 172:853-66, 1990; Essar <i>et al.</i> , J. Bacteriol., 172:867-83, 1990.
MUT2	ATP sulfurylase small subunit (CysD; PA4443)	Leyh <i>et al.</i> , J. Biol. Chem., 263:2409-16, 1988; Hummerjohann <i>et al.</i> , Microbiology, 144 (Pt 5):1375-86, 1998
MUT3	CysQ (PA5175)	Peng and Verma, J. Biol. Chem., 270:29105-10, 1995; Neuwald <i>et al.</i> , J. Bacteriol., 174:415-25, 1992.
MUT4	D-amino acid dehydrogenase, small subunit (dadA; PA5304)	Lobacka <i>et al.</i> , J. Bacteriol., 176:1500-10, 1994.
MUT5	imidazoleglycerol-phosphate synthase, cyclase subunit (hisF1; PA5140)	Fani <i>et al.</i> , Mol. Gen. Genet., 216:224-9, 1989; Fani <i>et al.</i> , Mol. Gen. Genet., 216:224-9, 1989.
MUT6	N-acetyl- γ -glutamyl-phosphate reductase (ArgC; PA0662)	Smith <i>et al.</i> , Gene, 49:53-60, 1986.
MUT7	Dihydrolipoamide acetyltransferase (AceF; pyruvate dehydrogenase complex component E2; PA5016)	Rae <i>et al.</i> , J. Bacteriol., 179:3561-71, 1997.
MUT8	NADH dehydrogenase I chain H (nuoH; PA2643)	Weidner <i>et al.</i> , J. Mol. Biol., 5:233:109-22, 1993; Weidner <i>et al.</i> , J. Mol. Biol., 233:109-22, 1993.
MUT9	pyoverdine synthetase D (PvdD; PA2399)	Rombel <i>et al.</i> , Mol. Gen. Genet., 246:519-28, 1995; Merriman <i>et al.</i> , J. Bacteriol., 177:252-8, 1995.
MUT10	RND multidrug efflux transporter MexD (mexD; PA4598)	Poole <i>et al.</i> , Mol. Microbiol., 21:713-24, 1996; Poole <i>et al.</i> , Mol. Microbiol., 21:713-24, 1996.
MUT11	PA3721	Stover <i>et al.</i> , Nature, 406:959-964, 2000.
MUT12	PA0596	Tan <i>et al.</i> , Proc. Natl. Acad. Sci. USA, 96:2408-13, 1999.
MUT13	PA5265	Stover <i>et al.</i> , Nature, 406: 959-964, 2000.

MUT14	pyochelin biosynthetic protein pchC (PA4229)	Serino <i>et al.</i> , Mol. Gen. Genet., 249: 217-28, 1995; Serino <i>et al.</i> , J. Bactiol., 179:248-57, 1997
MUT15	dihydroaeruginosic acid synthetase (pchE; PA4226)	Reimmann <i>et al.</i> , Microbiology, 144: 3135-48, 1998.
MUT16	Pyochelin synthetase (pchF; PA4225)	Reimmann <i>et al.</i> , Microbiology, 144: 3135-48, 1998.
MUT17	ATP-binding component of the ABC transporter (pchH; PA4223)	Featherston <i>et al.</i> , Mol. Microbiol., 32(2):289-99, 1999; Reimmann <i>et al.</i> , J. Bacteriol., 183:813-20, 2001.
MUT18	ATP-binding component of the ABC transporter (pchI; PA4222)	Reimmann <i>et al.</i> , J. Bacteriol., 183:813-20, 2001.
MUT19	putative O-antigen biosynthesis gene cluster	Rocchetta <i>et al.</i> , Microbiol. Mol. Biol. Rev. 63:523-53, 1999.

The 27 *Klebsiella* attenuated MUTX organisms harboring the VIRX genes disclosed in the present invention and assigned a new role in virulence are summarized below in Table 2.

5

Table 2

STRAIN	AFFECTED VIRULENCE GENE(S)
MUT20	hypothetical transcriptional regulator in met G-dld intergenic region
MUT21	β -cystathionase
MUT22	ribosome binding factor A
MUT23	aspartokinase/homoserine dehydrogenase
MUT24	cystathionine γ -synthase
MUT25	Phosphoribosylformylglycinamide synthase

MUT26	homoserine transsuccinylase
MUT27	3'-phosphoadenosine 5'-phosphosulfate reductase
MUT28	Sfi protein
MUT29	transcriptional activator protein LysR
MUT30	TrpD
MUT31	N-acetylglucosamine-6-phosphate deacetylase
MUT32	WaaQ
MUT33	2-Isopropylmalate synthase
MUT34	histidinol dehydrogenase
MUT35	UDP-galactopyranose mutase
MUT36	O-antigen export system permease protein rfba
MUT37	uridyltransferase
MUT38	pyridoxine phosphate biosynthetic protein PdxJ-PdxA
MUT39	triose phosphate isomerase
MUT40	aldehyde dehydrogenase
MUT41	galactosyl transferase
MUT42	siroheme synthetase
MUT43	7,8-dihydro-6-hydroxymethylpterin-pyrophosphokinase
MUT44	glucose-6-phosphate isomerase
MUT45	DNA methylase
MUT46	putative inner membrane protein

II. ATTENUATED BACTERIAL MUTANTS

A. Attenuated *Pseudomonas aeruginosa* Mutants

MUT1

A *Pseudomonas* bacterial mutant (MUT1) was made by transposon insertion in a *P. aeruginosa* wild-type strain PT894. In the *Dictyostelium* growth assay, the mutated microorganism was less virulent compared to an isogenic bacterial strain. The nucleotide sequence immediately following the transposon insertion was cloned and identified as the gene encoding anthranilate phosphoribosyltransferase (PA0650). This gene encodes the VIR1 nucleic acid (SEQ ID NO:1) shown in Table 3A.

Table 3A. VIR1 Nucleotide Sequence (SEQ ID NO:1)

```
ATGGATATCAAGGGAGCCCTCAATCGCATCGTCAACCAGCTCGACCTGACCACCGAGGAAATGCAGG
CGGTCATGCGCCAGATCATGACCGGGCAGTGCACCGACGCGCAGATCGGCGCCCTTCCTGATGGGCAT
GCGGATGAAGAGCGAAACCATCGACGAGATCGTTCGGCGCGGTGGCGGTGATGCGCGAATGGCCGAC
GGCGTGCAAGTTGCCACGCTGAAGCATGTGGTCGACGTGGTCGGCACCGGCGGCGATGGCGCGAACA
TCTTCAACGTGTCTCGGCGGGCTCCCTTCGTGGTCGCCGCCGCTGGCGGCAAGGTCGCCAAACACGG
TAACCGCGCGGTCTCCGGCAAGAGCGGCAGCGCCGACTTGTGGAAGCCGCCGCGCATCTACCTGGAG
CTGACCTCCGAACAGGTGGCGCGTTCGATCGACACCGTCGGCGTCGGGTTCATGTTGCCCCAGGTCC
ACCACAAGGCGATGAAGTACGCGCGCGGTCCGCGCCGCGAGCTGGGCTTGCGGACTCTGTTCAACAT
GCTTGGCCCACTGACCAACCCGGCGGGAGTCAGGCACCAGGTGGTCGGGTGTTTACCCAGGAAC TG
TGCAAGCCGCTGGCTGAAGTGTCAAGCGTCTCGGCAGCGAGCATGTGCTGGTGGTGCATTTCGCGCG
ACGGGCTGGACGAGTTTCAGTCTGGCCGCGCGGACCCACATTGCCGAGTTGAAGGACGGCGAGGTACG
CGAGTACGAAGTGGCTCCCGAGGACTTCGGGATCAAGAGCCAGACCTGATGGGGCTGGAGGTTCGAC
AGTCCGCAGGCCCTCGCTGGAACTGATCCGCGACGCTTTGGGGCGGCGCAAGACCGAGGCTGGGCAGA
AGGCCGCCGAGCTGATCGTGATGAATGCCGGCCCGGCACGTGTACGCTGCCGATCTGGCGACCAGCCT
GCACGAGGGCATTCAACTGGCCACGATGCCCTGCACACCGGGCTGGCACGGGAGAAGATGGACGAA
CTGGTGGCCTTACC CGCGTTTACAGAGAGGAGAACGCACAGTGA
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The VIR1 protein (SEQ ID NO:2) encoded by SEQ ID NO:1 is presented using the one-letter amino acid code in Table 3B.

Table 3B. Encoded VIR1 protein sequence (SEQ ID NO:2)

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MDIKGALNRIVNQLDLTTEEMQAVMRQIMTGQCTDAQIGAFLMGMRMKSETIDEIVGAVAVMREL
ADGVQLPTLKHVVDDVVGTTGGDGANIFNVSSAASFVVAAGGKVAKHGNRAVSGKSGSADLLEAAG
IYLELTSEQVARCIDTVGVGFMFAQVHHKAMKYAAGPRRELGLRTLGNMLGPLTNPAGVRHQVVG
VFTQELCKPLAEVLKRLGSEHVLVHRSRDGLDEFSLAAATHIAELKDGEVREYEVRPEDFGIKSQ
TLMGLEVDSPQASLELIRDALGRRKTEAGQKAAELIVMNAGPALYAADLATSLHEGIQLAHDALH
TGLAREKMDDELVAFTAVYREENAQ
```

The role of VIR1 in virulence was confirmed using phage to retransduce this mutation into the wild-type PT894 strain where attenuated virulence was again observed in the *Dictyostelium* growth assay compared to an isogenic bacterial strain.

MUT2

A *Pseudomonas* bacterial mutant (MUT2) was made by transposon insertion in a *P. aeruginosa* wild-type strain PT894. In the *Dictyostelium* growth assay, the mutated microorganism was less virulent compared to an isogenic bacterial strain. The nucleotide sequence immediately following the transposon insertion was cloned and identified as the gene encoding the ATP sulfurylase small subunit (CysD; PA4443). This gene encodes the VIR2 nucleic acid (SEQ ID NO:3) shown in Table 4A.

Table 4A. VIR2 Nucleotide Sequence (SEQ ID NO:3)

```

ATGGTCGACAACTGACGCACCTGAAACAGCTGGAGGCGGAAAGCATCCACATCATCCGCGAGGTGG
CCGCCGAGTTCGATAACCCGGTGATGCTGTACTCGATCGGCAAGGATTCCGCGGTTCATGCTGCACCT
GGCCCGCAAGGCCTTCTTCCCGGCAAGCTGCCCTTCCCGGTGATGCACGTGGACACCCGCTGGAAA
TTCCAGGAGATGTACAGGTTCGGTGATCGGATGGTCGAGGAAATGGGCCCTGGATCTGATCACCCACG
TCAACCCGGACGGCGTCGCCCAGGGCATCAACCCGTTACCCACGGCAGCGCCAAGCACACCGACGT
GATGAAGACCGAGGGACTCAAGCAGGCCCTGGACAAGTACGGTTTCGACGCTGCCCTTCGGCGGTGCG
CGCCGCGACGAGGAGAAGTCGCGGGCCAAGGAACGGGTCATTCGTTCCGCGACAGCAAGCACCGCT
GGGACCCGAAGAACCAGCGTCCCGAGCTGTGGAACATCTACAACGGCAAGGTGAAGAAGGGCGAGTC
GATCCGCGCTCTTCCCGCTGTCCAAC TGGACCGAGCTGGACATCTGGCAATACATCTACCTGGAAGGC
ATCCCGATCGTCCCGCTGTACTTCGCCGCCGAGCGCGAGGTCATCGAGAAGATGGCACATTGATCA
TGATCGACGACGAGCGCATCCTCGAGCATCTCTCTGACGAAGAGAAAGCCCGCATCGAGAAGCGCAT
GGTGCGCTTCCGTACCCCTCGGCTGCTACCCGCTCACC GGCGCGGTTCGAGTCCAGCGCCACCACGCTG
CCGAAATCATCCAGGAAATGCTCCTGACGCGTACTTCCGAACGCCAGGGCCGGGTCATCGACCATG
ACCAGGCCGGTTCGATGGAAGAAAAGAAACGTCAGGGCTATTTCTGA

```

The VIR2 protein (SEQ ID NO:4) encoded by SEQ ID NO:3 is presented using the one-letter amino acid code in Table 4B.

Table 4B. Encoded VIR2 protein sequence (SEQ ID NO:4)

```

MVDKLTHLKQLEAESIHIREVAAEFDPVMLYSIGKDSAVMLHLARKAFFPGKLPFPVMHVDTR
WKFQEMYRFRDRMVEEMGLDLITHVNPDGVAQGINPFTHGS AKHTDVMKTEGLKQALDKYGFDA
FGGARDEEKSRAKERVYSFRDSKHRWDPKNQRP ELWNIYNGKVKKGESIRVFPLSNWTELDIWQ
YIYLEGIPIVPLYFAAEREVIEKNGT LIMIDDERILEHLSDEEKARIEKRMVRFRTLGCYPLTGA
VESSATTLPEIIQEMLLTRTSERQGRVIDHDQAGSMEEKRQGYF

```

The role of VIR2 in virulence was confirmed using phage to retransduce this mutation into the wild-type PT894 strain where attenuated virulence was again observed in the *Dictyostelium* growth assay compared to an isogenic bacterial strain.

MUT3

A *Pseudomonas* bacterial mutant (MUT3) was made by transposon insertion in a *P. aeruginosa* wild-type strain PT894. In the *Dictyostelium* growth assay, the mutated

microorganism was less virulent compared to an isogenic bacterial strain. The nucleotide sequence immediately following the transposon insertion was cloned and identified as the gene encoding CysQ (PA5175). This gene encodes the VIR3 nucleic acid (SEQ ID NO:5) shown in Table 5A.

5

Table 5A. VIR3 Nucleotide Sequence (SEQ ID NO:5)
ATGAGGCCGGTGCCTTGGGGCGAATTGGTGGCGCTGGTGCGGCGCGCCGGCGAGGCGATCCTGCCGC ACTGGCGCGCCGACGTGGTGGTGGCTCGAAGGCCGACGAATCGCCGGTGACTGCCGCCGACCTGGC CGCGCACCATATATTGGAGCGGGATTGCGGGCGCTGGCGCCGACATTCCGGTGCTTTCCGAAGAG GATTGCGAGATACCGCTGAGCGAGCGCGCCACTGGCGGGCGCTGGTGGCTGGTGGACCCGCTGGACG GCACCAAGGAGTTCATCTCCGGTAGCGAGGAGTTCACCGTCAACGTGGCCCTGGTCGAGGATGGCCG GGTGCTGTTTCGGCCTGGTTCGGCGTGCCGGTGAGCGGCCGCTGCTACTACGGTGGCGCCGGTCTCGGT GCCTGGCGCGAGGAGGCCGATGGCCGCGCGCAACCGATCAGTGTGCGCCTGGAGCCCGAGGAGGCCT TCACCGTGGTGGCCAGCAAGCGCCATGGCAGCCCGGCCAGGAGCGCCTGCTGGATGGCTTGAGCGA GCGCTTCGGCGACCTGCGGCGAGCCAGCATCGGCAGTTCGCTGAAGTTCGCTGCTGGCCGAGGGC GTGCCGACTGCTATCCGCGCCTGACGCCAACCTCGCAATGGGACACGGCCGCCCGCCAGGGTGTGC TGGGAAGGCGCCGCGGCGAGGTGCTCGACCTGCATGGTGGCCATTACCTACGAGCCGCGCGAGGA TTACCTCAACGGCTCCTTCTGGCCCTGCCGCGCGCCCGAGTGGCGCAGCGAGCTGATCCAACCTG GCGCGCGCGCTGCACTGA

The VIR3 protein (SEQ ID NO:6) encoded by SEQ ID NO:5 is presented using the one-letter amino acid code in Table 5B.

Table 5B. Encoded VIR3 protein sequence (SEQ ID NO:6)
MRPVPWGELVALVRRAGEAILPHWRADVVRKSKADESPVTAADLAHHILEAGLRALAPDIPVLS EEDCEIPLSERGHWRRLVLDPLDGTKEFISGSEFTVNVALVEDGRVLFGLVGVVPSGRCCYYGG AGLGAWREEADGRAQPI SVRLEPEEAFTVVASKRHGSPAQERLLDGLSERFGDLRRASIGSSLKF CLLAEGAADCYPRLTPTSQWDTAAAGVLEAGGEVLDLHGAPFTYEPREDYLNGLALPRAAE WRSELIQLARALH

10

MUT4

A *Pseudomonas* bacterial mutant (MUT4) was made by transposon insertion in a *P. aeruginosa* wild-type strain PT894. In the *Dictyostelium* growth assay, the mutated microorganism was less virulent compared to an isogenic bacterial strain. The nucleotide sequence immediately following the transposon insertion was cloned and identified as the gene encoding D-amino acid dehydrogenase, small subunit (dadA; PA5304). This gene encodes the VIR4 nucleic acid (SEQ ID NO:7) shown in Table 6A.

15

Table 6A. VIR4 Nucleotide Sequence (SEQ ID NO:7)
ATGCGAGTTCTGGTCCTTGGCAGCGGTGTCATCGGTACCGCCAGTGCGTATTACCTGGCCCCGTGCCG GGTTCGAGGTGGTGGTGGTCGACCGTCAGGACGGTCCCGCGCTGGAAACCAGCTTCGCCAACGCCGG

```

CCAGGTGTCTCCCGGCTACGCTTCGCCCTGGGCAGCCCCGGGCATTCCCCTGAAGGCCATGAAGTGG
CTGCTGGAAAAGCACGCGCCGCTGGCCATCAAGCTCACCTCCGATCCCAGCCAGTACGCCCTGGATGC
TGCAGATGCTGCGCAACTGCACCGCCGAGCGCTACGCCGTGAACAAGGAGCGCATGGTCCGCCCTGTC
CGAGTACAGCCGCGATTGCCCTCGACGAACTGCGCGCCGAGACCGGCATCGCCTACGAGGGCCGCACC
CTCGGCACCACTTGTTCGCGACCCAGGCGCAGCTGGACGCCGCCGGCAAGGACATCGCCGTGC
TCGAGCGCTCCGGCGTGCCCTACGAGGTTCTCGACCGCGACGGCATCGCCCGCTAGAGCCGGCTTT
GGCCAAGGTCGCCGACAAGCTGGTCGGCGCCTTGCGCCTGCCCAACGACCAGACCGCGACTGCCAG
CTGTTTACCACCCGCCCTGGCGGAAATGGCCAAGGGCTGGGCGTGGAGTTCCGCTTCGGCCAGAACA
TCGAGCGCCTGGACTTCGCCGGCGACCGCATCAACGGCGTGCTGGTCAACGGCGAATTGCTCACC GC
CGACCACTACGTGCTGGCCCTGGGCAGCTACTCGCCGCAACTGCTCAAGCCGCTGGGTATCAAGGCT
CCGGTCTATCCGCTGAAGGGTTATTCGCTGACCGTGCCGATCACCACCCGGAGATGGCGCCGACCT
CGACCATCCTCGACGAGACCTACAAGGTGGCGATCACC CGCTTCGACCAGCGCATCCGCGTCGGCGG
CATGGCGGAAATCGCCGGCTTCGACCTGTCGCTGAACCCGCGCCGCGCGAGACCCCTGGAAATGATC
ACCACCGACCTCTATCCCAGGGCGGCGATATCAGCCAGGCGACCTTCTGGACCGGCCCTGCGCCCGG
CGACCCCGGATGGCACCCCGATCGTCGGCGCCACCCGCTACCGCAACCTGTTCTCAATACCGGCCA
CGGCACCTTGGGTTGGACCATGGCCTGCGGGTTCGGTTCGCTACCTGGCCGACCTGATGGCGAAGAAG
CGCCCGCAGATCAGTACCGAAGGCTGGATATTCCCGCTACAGCAATTCCCCGGAGAACGCCAAGA
ATGCCCATCCAGCGCCAGCACACTAA

```

The VIR4 protein (SEQ ID NO:8) encoded by SEQ ID NO:7 is presented using the one-letter amino acid code in Table 6B.

Table 6B. Encoded VIR4 protein sequence (SEQ ID NO:8)

```

MRVLVLGSGVIGTASAYYLARAGFEVVVVDRQDGPALETSFANAGQVSPGYASPWAAPGIPLKAM
KWLLEKHAPLAIKLTSDPSQYAWMLQMLRNCTAERYAVNKMVRLSEYSRDCLDELRAETGIAY
EGRTLGTTLQFLRTQAQLDAAGKDIAVLERSGVPEVLDRDGIARVEPALAKVADKLVGALRLPND
QTGDCQLFTTRLAEMAKGLGVEFRFGQNIERLDFAGDRINGVLVNGELLTADHYVLALGSYSPQL
LKPLGIKAPVYPLKGYSLTVPITNPEMAPTSTILDETYKVAITRFQRIRVGGMAEIAFGDLSLN
PRRRETLEMITTDLYPEGDISQATFWTGLRPATPDGTPIVGATRYRNLFLNTGHGTLGWTMACG
SGRYLADLMAKKRPQISTEGLDISRYSNSPENAKNAHPAPAH

```

The role of VIR4 in virulence was confirmed using phage to retransduce this mutation into the wild-type PT894 strain where attenuated virulence was again observed in the *Dictyostelium* growth assay compared to an isogenic bacterial strain.

MUT5

A *Pseudomonas* bacterial mutant (MUT5) was made by transposon insertion in a *P. aeruginosa* wild-type strain PT894. In the *Dictyostelium* growth assay, the mutated microorganism was less virulent compared to an isogenic bacterial strain. The nucleotide sequence immediately following the transposon insertion was cloned and identified as the gene encoding imidazoleglycerol-phosphate synthase, cyclase subunit (hisF ; PA5140). This gene encodes the VIR5 nucleic acid (SEQ ID NO:9) shown in Table 7A.

Table 7A. VIR5 Nucleotide Sequence (SEQ ID NO:9)

```

ATGGCACTGGCAAACGCATCATCCCCTGCCTCGACGTGGACAACGGCCGAGTGGTCAAGGGCGTCA

```

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AGTTCGAGAACATCCGCGACGCCGGCGACCCGGTCGAGATCGCTCGCCGCTACGACGAGCAGGGTGC
CGACGAGATCACCTTCCTCGATATCACGCCAGCGTCGACGGGCGCGACACCACCCTGCATACCGTC
GAGCGCATGGCTAGCCAGGTGTTTATTCCGCTGACCGTGGGCGGCGCGGTACGCGAGCGTGCAGGACA
TCCGCAACCTGTTGAATGCCGGCGCGGACAAGGTCTCGATCAACACCGCCGCGGTGTTCAACCCCGA
GTTTCGTCGGTGAGGCCGCCGACCGCTTCGGCTCGCAGTGCATCGTGGTCCGATCGACGCGAAGAAG
GTTTCGCCCCCGGCGAGGCCGCCGCTGGGAAATCTTACCCATGGCGGGCGCAAGCCCACCGGGC
TGGATGCCGTGCTCTGGGCGAAGAAGATGGAAGACTTGGGCGCTGGCGAGATTCTCCTGACCAGCAT
GGACCAGGACGGCGTGAAGAGCGGTTACGACCTGGGCGTGACCCGCGCCATCAGCGAGGCGGTGAAC
GTGCCGGTGATCGCTTCCGGCGGCGTCGGCAACCTGGAGCACCTGGCCGCCGGCATCCTCGAGGGCA
AGGCCGACGCGGTGCTCGCGGCGAGCATCTTCCACTTCGGCGAGTACACCGTGCCGGAAGCCAAGGC
CTACCTGGCCAGCCGCGGTATCGTGGTGCGCTGA

```

The VIR5 protein (SEQ ID NO:10) encoded by SEQ ID NO:9 is presented using the one-letter amino acid code in Table 7B.

Table 7B. Encoded VIR5 protein sequence (SEQ ID NO:10)

```

MALAKRIIPCLDVDNGRVVKGKVFENIRDAGDPVEIARRYDEQGADEITFLDITASVDGRDRTLH
TVERMASQVFIPLTVGGGVRSVQDIRNLLNAGADKVSINTAAVFNPEFVGEAADRFSGQCI VVAI
DAKKVSAPGEAPRWEIFTHGGRKPTGLDAVLWAKKMEDLGAGEILLTSMQDGVKSGYDLGVTRA
ISEAVNVFVIASGGVGNLEHLAAGILEGKADAVLAASIFHFGEYTVPEAKAYLASRGIVVR

```

MUT6

A *Pseudomonas* bacterial mutant (MUT6) was made by transposon insertion in a *P. aeruginosa* wild-type strain PT894. In the *Dictyostelium* growth assay, the mutated microorganism was less virulent compared to an isogenic bacterial strain. The nucleotide sequence immediately following the transposon insertion was cloned and identified as the gene encoding N-acetyl-•-glutamyl-phosphate reductase (ArgC; PA0662). This gene encodes the VIR6 nucleic acid (SEQ ID NO:11) shown in Table 8A.

Table 8A. VIR6 Nucleotide Sequence (SEQ ID NO:11)

```

ATGATCAAGGTCGGCATCGTTGGCGGTACGGGTTATACGGGCGTGGAAGTCTGCGCCTGCTGGCGC
AGCATCCGCAGGCCCGGGTGGAAAGTGATCACTTCGCGTTCCGAGGCGGGGGTGAAGGTCGCCGACAT
GTACCCGAACCTGCGAGGTCATTATGACGACCTGCAGTTCAGCGTGCCGGACGCGCAGCGCCTCGGC
GCCTGCGACGTGGTGTTCTTCGCCACGCCGACGGCGTGCGCACGCGCTGGCTGGCGAACTGCTGG
ACGCCGGGACCCGGGTCATCGATCTGTCCGCTGACTTCCGCCTGGCGGACGCCGAGGAGTGGGCGCG
CTGGTACGGCCAGCCGATGGCGCTCCGGCGCTGCTCGACGAGGCTGTCTACGGCCTGCCGGAAGTG
AACC GCGAGAAGATCCGCCAGGCCCGCCTGATCGCCGTGCCGGGCTGCTACCCGACCGCGACCCAGC
TGGGCTGATCCCGCTGCTGGAAGCCGGCCTGGCCGACGCTCGCGGCTGATCGCCGATTGCAAGTC
CGGGGTCAGCGGTGCCGGTCGGGGCGCCAAGGTTGGCTCGCTGTCTCGAGAGCGGGCGAAAGCATG
ATGGCTACGCGGTCAAAGGGCATCGGCATCTCCCGAAATCAGCCAGGGCCTGCGTCGGGCTCCG
GCGGCGACGTCGGGCTGACGTTCTGACCGCACCTGACGCCAATGATCCGCGGTATCCATGCAACCTT
CTATGCCCATGTGCGGGATCGCTCGGTGACCTCCAGGCGTTGTTTCGAGAAGCGCTACGCCGACGAA
CCCTTCGTCGACGTGATGCCGGCCGGCAGCCATCCGGAGACCCGACGCTGCGTGCGGCGCAATGTCT
GCCGAATCGCCGTGATCGCCCCAGGGCGGCGACCTGGTGGTGGTGCTGTGCGGTGATCGACAACCT
GGTCAAGGGCGCCTCGGGTCAGGCTCCAGAACATGAACATCCTGTTCCGGGCTGGACGAGCGCCTG
GGCCTCTCGCATGCGGCCCTGCTCCCTGA

```

The VIR6 protein (SEQ ID NO:12) encoded by SEQ ID NO:11 is presented using the one-letter amino acid code in Table 8B.

Table 8B. Encoded VIR6 protein sequence (SEQ ID NO:12)

MIKVGIVGGTGYTGVELLRLLAQHPQARVEVITSRSEAGVKVADMYPNLRGHYDDLQFVSPDAQR
LGACDVVFFATPHGVAHALAGELLDAQTRVIDLSADFRADAEWARWYGQPHGAPALLDEAVYG
LPEVNREKIRQARLIAVPGCYPTATQLGLIPLLEAGLADASRLIADCKSGVSGAGRGAKVGSFLC
EAGESMMAYAVKGRHLPETISQGLRRASGGDVGLTFVPHLTPMIRGIHATLYAHVADRSVDLQAL
FEKRYADEPFVDVMPAGSHPETRSVRGANVCRIAVHRPQGGDLVVVLSVIDNLVKGASGQALQNM
NILFGLDERLGLSHAALLP

- 5 The role of VIR6 in virulence was confirmed using phage to retransduce this mutation into the wild-type PT894 strain where attenuated virulence was again observed in the *Dictyostelium* growth assay compared to an isogenic bacterial strain.

MUT7

- 10 A *Pseudomonas* bacterial mutant (MUT7) was made by transposon insertion in a *P. aeruginosa* wild-type strain PT894. In the *Dictyostelium* growth assay, the mutated microorganism was less virulent compared to an isogenic bacterial strain. The nucleotide sequence immediately following the transposon insertion was cloned and identified as the gene encoding dihydrolipoamide acetyltransferase (AceF; PA5016). This gene encodes the VIR7 nucleic acid (SEQ ID NO:13) is shown in Table 9A.

Table 9A. VIR7 Nucleotide Sequence (SEQ ID NO:13)

GTGAGCGAACTCATTTCGCGTACCCGACATCGGCAACGGTGAGGGTGAAGTCATCGAGCTGCTGGTCA
AGCCCGCGACAAGGTCGAGGCCGATCAGAGCCTGCTGACCCTGGAATCCGACAAGGCCAGCATGGA
AATCCCCAGTCCCAAGGCCGGGGTAGTGAAAAGCATCAAGGCGAAGGTCGGCGACACCTTGAAAGAA
GGTGACGAAATCTCGAGCTGGAAGTGGAAGGCGGCGAACAGCCTGCCGAAGCCAAGGCCGAGGCAG
CGCCCGCCCAACCGGAAGCGCCGAAAGCCGAAGCGCCTGCTCCCGCCCCGAGCGAGAGCAAGCCGGC
CGCCCCCGCGCGGCCAGCGTCCAGGACATCAAGGTCCCGGACATCGGCTCGGCCGGCAAGGCCAAC
GTCATCGAAGTGATGGTCAAGGCCGGCGACACGGTCGAGGCCGACCAGTCGCTGATCACCCTGGAAT
CCGACAAGGCCAGCATGGAGATCCCCCTCGCCGGCCTCCGGGGTGTTGGAAAGCGTCTCGATCAAGGT
CGGTGACGAAGTCGGCACCGGCGACCTGATCCTCAAGCTGAAGGTGGAAGGCGCCGCTCCGGCAGCC
GAAGAGCAACCGGCAGCCGCTCCCGCCAGGCCGCGCGCCCGCCGAGCAGAAGCCCGCCGCGG
CGGCCCTGCGCCAGCCAAGGCCGATACCCCGGCTCCGGTCGGCGCACCCAGCCGCGACGGCGCCAA
GGTCCACGCCGGCCCCGGCGGTGCGCATGCTGGCGCGCGAGTTTCGGCGTCGAGCTGAGCGAAGTGAAA
GCCAGCGGTCCCAAGGGTCGCATCCTCAAGGAAGACGTCCAGGTCTTCGTCAAGGAGCAACTGCAGC
GCGCCAAGTCCGGCGGTGCCGGCGCCACCGGCGGAGCCGGCATCCCGCCGATCCCGGAAGTCGACTT
CAGCAAGTTCGGCGAAGTGGAAGAAGTGCGCATGACCCGCTGATGCAGGTTCGGCGCCGCCAACCTG
CATCGCAGCTGGCTGAACGTGCCGCACGTGACCCAGTTCGACCATCGGACATCACCGACATGGAAG
CCTTCCCGCTTGCCGAGAAGGCCGCGGCGGAGAAGGCCGGGTCAAGCTGACCGTACTGCCGATCCT
GCTCAAGGCCTGCGCCACCTGCTCAAGGAAGTCCCGGACTTCAACAGTTTCGCTGGCCCCAGCGGC
AAGGCGCTGATCCGCAAGAAGTACGTACACATCGGCTTCGCCGTGGACACTCCGGACGGCCTGCTGG
TCCCGGTGATCCCGCATGTCGACCGGAAGAGCTCCTGCAACTGGCCGCCGAGGCCGCCGACCTGGC
CGACAAGGCCCGCAACAAGAAGCTCTCGGCCGATGCCATGCAGGGCGCCTGCTTACCATCTCCAGT
CTCGGCCACATCGGCCGACCGGCTTACGCCGATCGTCAACGCGCCGGAAGTGGCGATCCTCGGTG

TGTCCAAGGCGACCATGCAGCCGGTATGGGACGGCAAGGCCTTCCAGCCGCGCCTGATGCTGCCGCT
 GTCGCTGTCTACGACCATCGCGTGATCAACGGTGCCGCGCGCGCTTCACCAAGCGCCTGGGC
 GAGCTGCTGGCGGACATCCGCACCCTGCTCCTGTAA

The VIR7 protein (SEQ ID NO:14) encoded by SEQ ID NO:13 is presented using the one-letter amino acid code in Table 9B.

Table 9B. Encoded VIR7 protein sequence (SEQ ID NO:14)

MSELIRVPDIGNGEGEVIELLVKPGDKVEADQSLITLES DKASMEIPSPKAGVVKSIAKAVGDTL
 KEGDEILELEVEGGEQPAEAKAEAAPAQPEAPKAEAPAPAPSESKPAAPAAASVQDIKVPDIGSA
 GKANVIEVMVKAGDTVEADQSLITLES DKASMEIPSPASGVVESVSIKVGDEVGTGDLILKLKVE
 GAAPAAEEQPAAPAAQAAAPAAEQKPAAAAAPAKADTPAPVGAPSRDGAKVHAGPAVRMLAREF
 GVELSEVKASGPKGRILKEDVQVFVKEQLQRAKSGGAGATGGAGIPPIPEVDFSKFGEVEEVAMT
 RLMQVGAANLHRSWLNVPVHTQFDQSDITDMEAFRVAQKAAAEKAGVKLTVLPILLKACAHLLKE
 LPDFNSSLAPSGKALIRKKYVHIGFAVDTPDGLLVPIRDVDRKSLQLAAEAADLADKARNKKL
 SADAMQGACFTISSLGHIGGTGFTPIVNAPEVAILGVSKATMQPVWDGKAFQPRMLPLSLSYDH
 RVINGAAAARFTKRLGELLADIRTL

MUT8

A *Pseudomonas* bacterial mutant (MUT8) was made by transposon insertion in a *P. aeruginosa* wild-type strain PT894. In the *Dictyostelium* growth assay, the mutated microorganism was less virulent compared to an isogenic bacterial strain. The nucleotide sequence immediately following the transposon insertion was cloned and identified as the gene encoding NADH dehydrogenase I chain H (nuoH; PA2643). This gene encodes the VIR8 nucleic acid (SEQ ID NO:15) shown in Table 10A.

Table 10A. VIR8 Nucleotide Sequence (SEQ ID NO:15)

ATGAGTTGGCTGACTCCCGCTCTGGTCACCATCATCCTCACCGTGGTCAAGGCCATCGTGGTGCTGC
 TCGCCGTGGTCATCTGCGGCGCCCTGCTAAGCTGGGTGCGAGCGCCGCTGCTCGGCCTCTGGCAGGA
 CCGCTACGGCCCCAACC GGTCGGTCCGTTCCGTTCCAGCTCGGCGCGGACATGGTCAAGATG
 TTCTTCAAGGAGGACTGGACCCCGCCGTTCCGCCGACAAGATGATCTTCACCTGGCCCCGGTAATCG
 CGATGGGCGCCCTGCTCGCTCGCCTTCGCCATCGTGCCGATCACCCCCACCTGGGGCGTGGCGGACCT
 GAACATCGGCATCCTGTCTTCTTCGCCATGGCCGCGCTGACGGTGACGCCGTGCTGTTCGCCGCG
 TGGTCGAGCAACAAGTTCGCCCTGCTCGGCAGCCTGCGCGCCTCGGCCAGACCATCTCCTACG
 AGGTGTTCTTGGCCCTGTCGCTGATGGGCATCGTCGCCAGGTCGGCTCGTTCAACATGCGCGACAT
 CGTCCAGTACCAGATCGACAACGCTCGGTTTCATCATTCGCGAGTTCTTCGGCTTCTGCACCTTCATC
 ATCGCCGGCGTCGCCGTGACCCACCGTCACCCGTTTCGACCAGCCGGAAGCGGAGCAGGAACCTGGCGG
 ACGGCTACCACATCGAGTACGCCGGGATGAAATGGGGCATGTTCTTCGTCGGCGAGTACATCGGCAT
 CGTACTGGTCTCGGCGCTGCTGGCGACCCTGTTCTTCGGCGGCTGGCACGGTCCGTTCTTGACACC
 CTGCCCTGGCTGCTGTTCTTCTACTTCGCCGCAAGACCGGCTTCTTCATCATGCTCTTCATCCTGA
 TCCGCGCCTCGCTGCCGCGTCCGCGCTATGACCAGGTGATGGCGTTACGCTGGAAGGTGCGCTGCC
 GCTGACCTGATCAACCTGCTGGTGACCGCGCGCTCGTGCTGGCCGCGGCCAGTAA

The VIR8 protein (SEQ ID NO:16) encoded by SEQ ID NO:15 is presented using the one-letter amino acid code in Table 10B.

Table 10B. Encoded VIR8 protein sequence (SEQ ID NO:16)

MSWLTPLALVTIILTUVVKAIVVLLAVVICGALLSWVERRLLGLWQDRYGNRVGPFQAFQLGADMV
KMFFKEDWTPPFADKMIFTLAPVIAMGALLVAFIAIVPITPTWGVADLNIGILFFIFAMAGLTVYAV
LFAGWSSNNKFALLGSLRASAQTISYEVFLALSMLGIVAQVGSFNMRDIVQYQIDNVWFIIIPQFF
GFCTFIIAGVAVTHRHFPDQPEAEQELADGYHIEYAGMKWGMFFVGEYIGIVLVSALLATLFFGG
WHGPFDLTLPWLSFFYFAAKTGFFIMLFILIRASLPRPRYDQVMAFSWKVCLPLTLINLLVTGAL
VLAAAQ

5 MUT9

A *Pseudomonas* bacterial mutant (MUT9) was made by transposon insertion in a *P. aeruginosa* wild-type strain PT894. In the *Dictyostelium* growth assay, the mutated microorganism was less virulent compared to an isogenic bacterial strain. The nucleotide sequence immediately following the transposon insertion was cloned and identified as the gene encoding pyoverdine synthase D (PvdD; PA2399). This gene encodes the VIR9 nucleic acid (SEQ ID NO:17) shown in Table 11A.

Table 11A. VIR9 Nucleotide Sequence (SEQ ID NO:17)

GTGCAAGCACTCATAGAGAAGGTGGGCTCCCTTTCCCCCAGGAAAGGAAGGCATTGGCTGTCTGC
TCAAGCAGCAAGGTGTCAATCTCTTCGAGATCGCGCCAGTGTTCAGCGCCAGGACGGCGAGCCCCCT
GCGGCTCTCCTATGCCAGGAGCGACAGTGGTTTCTCTGGCAACTGGAGCCGGAAGCGCGGCTAC
CATATCCCGAGTGTCTTGCCTTACGTGGGCGGCTGGACCTGGATGCCCTGCAACGCAGCTTCGACA
GCCTGGTTCGCGGCGACGAGACCCCTACGCACCCGTTTTCGCTCGACGGCGACGAGGCGCGCCAGGA
GATCGCGCATCCATGGCATTTGCCGTTGGATATCGTCGCGTTGGGGCCGCTCGAGGAGGGCGCCCTC
GCTCGGCGAGTTCGAGACGACGATCGCGCGGCGGCTTCGACCTGGAGCGTGGGCGGCTGCTGCGGGTGA
GCCTGTTGCGGCTGGCCGAGGACGACCATGTGCTGGTGGTCCAGCATCACATCGTGTCCGACGG
TTGGTCGATGCAGGTGATGGTCGAGGAACGGTCCAGCTCTATGCCGCTATAGTCGAGGGCTCGAG
GTAGCGCTGCCGGCTTTGCCGATCCAGTACGCGGACTACGCCCTGTGGCAGCGCAGCTGGATGGAGG
CCGGGGAAGAGCGCCAGTTGGCGTACTGGACCGGCTGCTGGGCGGCGAGCAGCCGGTGTGGA
GTTGCCGTTTCGACCGGCCGCGCCCGGTTTCGGCAAAGCCATCGTGGTGGCCAGTTTCATCTGGAAGT
GATATTGATCTGTCCAGGCGCTCAGGCGCGTGGCCAGCAGGAGGGGGCTACTGCCTTCGCCCTGT
TGCTGGCTTCGTTCCAGGCGCTGCTGTATCGCTACAGCGGGCAGGCGGATATCCGTGTCGGCGTGCC
GATCGCCAATCGCAACCGCGTGGAGACCGAGCGGCTGATCGGCTTCTTCGTCAACACCCAGGTGCTC
AAGGCCGACCTGGACGGTTCGGATGGGCTTCGACGAGCTGCTGGCCAGGCCCCGCAACCGCGCTGG
AGGCCAGGCGCACCAGGACCTGCCGTTTCGACGAACTGGTGGAGGCCCTTGACGCCGAGCGCAGTCT
TAGCCACAACCCGCTGTTCAGGTGCTGTTCAACTACCAGAGCGAAGCCCGTGGCAACGCCAGGCA
TTCCGCTTCGACGAGTTACAGATGGAAAGCGTGCAGTTCGACAGCCGGACGGCGCAGTTCGACTTGA
CGTTGGACCTGACGGACGAAGAGCAGCGTTTTCGCGCCGTTTTCGACTACGCCACCGACCTGTTCGA
CGCTCCACCGTGGAAACGCTGGCCGGCCATTGGCGCAACCTGTTGCGCGGCATCGTCGCCAACCCA
CGACAGCGGCTCGGCGAGTTGCCGCTGCTGGATGCGCCGAGCGCGGAGCGCCGAGACCTCTCCGAATGGA
ACCGGCCAGCGCGAGTGCAGCGGTGCAGGGCACCTTGCAGCAGCGTTTCGAGGAACAGCGCGGCA
ACGGCCACAGGCGGTTGCGCTGATCCTCGACGAACAACGGTTGAGCTACGGCGAACTGAATGCGCGG
GCCAATCGCCTGGCGCACTGCCTGATCGCCCGTGGCGTTGGCGCGGACGTGCCGGTGGGCTGGCGC
TGGAGCGTTCGCTGGACATGCTGGTGGCTGCTGGCGATCCTCAAGGCCGGCGGCGCTACCTGCC
GTTGGACCGCGCGGCCAGAGGAGCGCTGGCGCATATCCTCGACGACAGTGGGGTACGGCTGCTG
CTGACCCAGGGCATCTGCTCGAGCGCTGCCACGGCAGGCGGGGTGGAGGTGCTGGCCATCGACG
GACTGGTGTGAGCGGCTACGCCGAGAGCATCGCTCCCGACGCTATCGGCGGACAACCTGGCCTA

CGTGATCTATACCTCGGGCTCGACCGGCAAGCCCAAGGGCACATTGCTCACCACCGCAACGCGCTG
CGCCTGTTACAGCGCCACCGAGGCTTGGTTCGGCTTCGACGAGCGGGACGTGTGGACATTGTTCCATT
CCTACGCTTCGATTCTCGGTCTGGGAAATCTTCGGCGCGCTGCTCTATGGCGGGTGCTTGGTAT
TGTGCCGCAATGGGTGAGCCGTTCGCCGGAAGACTTCTACCGTCTGCTGTGCCGCGAAGGCGTGACG
GTGCTCAACCAGACGCCGTTCGGCGTTCAGCAACTGATGGCGGTGGCTTCCGCCGACATGGCGA
CGCAGCAGCCGGCGCTGCGCTACGTGATCTTCGGTGGCGAGGCGCTGGATCTGCAGAGCCTGCGGCC
GTGGTTCAGCGCTTCGGCGATCGCCAGCCCAACTGGTGAACATGTACGGCATEACCGAGACCACG
GTGCACGTAACCTACCGTCCGGTGAGCGAGGCGGACCTGGAAGGTGGCTGGTCACTCCGATTGGCG
GGACCATCCCGGACCTGTCTGGTACATCTCGACCGTGACCTGAACCCGCTGCCGCGCGCGGT
GGGCGAGCTGTACATCGGTTCGCCCGGGCTGGCGCGCGGCTACCTGAGGCGGCGCGGTGAGTGCC
ACCCGCTTCGTGCCGAACCCGTTCGCCGGCGCGCGGCGAGCGGCTGTACCGTACCGGCGACCTGG
CACGGTTCAGGCGGATGGCAATATCGAGTACATCGGGCGTATCGACCACCGGTGAAGGTTCCGCG
CTTCGTATCGAACTGGGCGAGATCGAAGCGCGCTCGCCGCTTCGCCGGGTACGCGATGCCGTG
GTGCTGGCCCATGACGGAGTCGGCGGCACGCAACTGGTGGGATACGTGGTGGCGGACTCGGCGGAGG
ATGCCGAGCGTCTGCGGGAGTCGCTGCGGGAGTCGCTGAAGCGGCACCTGCCGGACTACATGGTGCC
GGCGACCTGATGCTGCTGGAGCGGATGCCGCTGACGGTCAATGGCAAGCTCGACCGGCAGGCGTTG
CCGCAACCGGATGCGAGCCTGTCGCAACAGGCTATCGAGCGCCCGGTAGCGAGCTGGAGCAGCGCA
TCGACGCGATCTGGTTCGAGATCTTGGGAGTGGAAACGGGTCGGCTGGACGACAACCTCTTCGAACT
GGGCGGTTCATTGCTTGGTACCGGGGTGATTTCTCGGGTTCGCCAGGAGCAGTGGACGCA
AGCCTGAAGGCGTTGTTGAGCGCGCGGTTCTGGAAGCGTTCGCCAGGGATTGGAACGCACGCG
ATGCTGCTCGACGATACCGCTTCGGATCGGCAGCAACCGTTGGCACTGTCTTCGCTCAGGAGCG
TCAGTGGTTCTCTGGCAACTGGAGCCGAAAGCGCGGCTACCATATTCCGAGTGCCTTGGCGCTA
CGCGGGCGGCTGGACGTGGATGCCTTGAACGCGAGCTTCGACAGCTGGTTCGCGCGGCGATGAAACCT
TGCGTACCGCTTCGGCTGGAGGGAGGCGTTCGTACAGCAGGTACAACCTGCGGTTAGCGTTTC
CATCGAGCGGGAACAGTTCCGGTGAAGAAGGCTGATCGAACGGATACAGGCCATCGTTGTGACGCCA
TTTCGACCTGGAACGGGGGCGCTGCTGCGGGTGAACCTGTTGCAACTGGCCGAGGACGACCATGTAC
TGGTGTGGTCCAGCACCACATCGTGTCCGATGGTGGTTCGATGTCAGGTGATGGTTCGAGGAACCTGGT
CCAGCTCTATGCCGCTATAGCCAAGGCTCGACGTGGTGGTGGTTCGAGCCTGCCGATCCAGTACGCG
GACTACGCCCTGTGGCAGCGCAGCTGGATGGAGGCGGGGAAAAGGAGCGCCAGTTGGCGTACTGGA
CCGGCCTGCTGGGCGGCGAGCAGCGGTGCTGGAGTTGCCGTTTCGATCGGCGCGGCTCCGGCCCGGCA
GAGCCATCGTGGCGCGCAGTTGGGTTTCGAGCTATCGCGGGAACCTGGTTCGAGGCGGTGAGAGCCTTG
GCCAGCGTGAAGGCGCCAGTAGTTTCATGCTGTTGCTGGCCTCGTTCCAGGCGCTGTTGTATCGCT
ACAGCGGGCAGGCGGATATCCGTGCTCGGTGTCGGATCGCCAATCGCAACCGCGTGGAGACCGAGCG
GCTGATCGGCTTCTTCGTCAACACCCAGGTGCTCAAGGCGGACCTGGACGGTTCGATGGGCTTCGAC
GAGCTGCTGGCCAGGCGCGCAACCGCGCTGGAGGCGCAGGCGCACCAGGACCTGCCGTTTCGAGC
AATGGTGAAGCCTTGCAGCGGAGCGCAATGCCAGCCACAACCCACTGTTCCAGGTGCTGTTCAA
CCATCAGAGCGAGATACGCTCGGTGACGCGCGAGGTTTCAGTTGGAGGACCTGCGTCTGGAAGGCGTG
GCCTGGGACGGCCAGACTGCGCAGTTTCGACCTGACGCTGGATATTCAGGAAGACGAAAACGGCATCT
GGGCTCTCTTCGACTATGCCACCGATCTGTTTCGACGCTTCACCGTGGAAACGCTGGCCGGCCATTG
GCGCAACCTGTTGCGCGGCGATCGTTCGCAACCCACGACAGCGGCTCGGCGAGTTGCCGCTGCTGGAT
GCGCGGAGCGCGGCGAGCCCTCTCCGAATGGAACCCGGCCAGCGCGAGTGGCGGTTGCGGCGGCA
CCTTGCAGCAGCGTTTCGAGGAGCAGGCGCGGCAACGGCCACAGGCGGTTGCGCTGATCTTCGACGA
ACAACGGTTGAGCTACGGCGAATGAAATGCGCGGGCCAAATCGCTGGCGCACTGCTGATCGCTCGC
GGCGTTGGCGCGGACGTGCCGCTGGGCTGGCGCTGGAGCGTTGCTGGACATGCTGGTGGCTTGC
TGGCGATCTCAAGGCGGCGGCGGCTACCTGCCGTTGGACCGGCGGCGCCAGAGGAGCGGCTGGC
GCATATCTTCGACGACAGTGGGGTACGGCTGCTGCTGACCCAGGGGCGATCTGCTCGAGCGCTTGGC
CGGAGGCGGGGGTGGAGGTGCTGGCCATCGACGGACTGGTGTGACGCGGCTACGCCGAGAGCGATC
CGCTCCCGACGCTATCGGCGGACAACCTGGCTTACGTGATCTATACCTCGGGCTCGACCGGCAAGCC
CAAGGGCAGCTTGTCAACCCACCGCAACGCGCTGCGCTGTTTCAGCGCCACCGAGGCTGCTTCGGC
TTCGACGAGCGGGACGTGTGGACGTTGTTCCATTCTACGCTTCGATTCTCGGTCTGGGAAATCT
TCGGCGCGCTGCTCTATGGCGGGCGCTGGTGTGCTGCGCAATGGGTGAGCGGTTGCCCGGAAGA
CTTCTACCGTCTGCTGTGCGCGAAGGCGTGACGGTGCTCAACAGACGCGCTGCGCTACGTGATCTTCG
CTGATGGCGGTGGCTGTTCCGCCGACATGGCGAGCAGCAGCCGGCGCTGCGCTACGTGATCTTCG
GTGGCGAGGCGCTGGATCTGCAGAGCCTGCGGCGGTGGTTCCAGCGCTTGGCGATCGCCAGCGCA
ACTGGTGAACATGTACGGCATCACCGAGACCAGGTACAGTAACCTACCGTCCGGTGAGCGAAGCC
GACCTGAAGGTGGCTGGTCACTCCGATCGGCGGGACCATCCCGGACCTGCTCTGGTACATCTCG
ACCGTGACCTGAACCCGTTGCCGCGCGCGGCTGGGCGAGCTGTACATCGGTGCGCGCGGTCTGGC
GCGCGGCTACCTGAGGCGGCGCGGCTTGAAGTGCACCCGCTTCGTGCCGAACCCGTTCCCGCGCGGT
GCCGCGGAGCGGCTGTACCGTACCGGCGACCTGGCACGGTTCCAGGCGGATGGCAATATCGAGTACA
TCGGGCGTATCGACCAACAGGTGAAGGTTTCGCGCTTCCGTATCGAACTGGGTGAGATCGAAGCGCG
GCTGCCGGTCTGGCCGGGTACGCGATGCCGTGGTGGTGGCCATGACGGGGTGGCGGCGACGCA
CTGGTGGGATACGTGGTGGCGGACTCGGCGGAGGATGCCGAGCGTCTGCCGGAGTGGTGGCGGAGT
CGCTGAAGCGGCACCTGCCGGACTACATGGTGGCGGCGACCTGATGCTGCTGGAGCGGATGCCGCT
GACGCTCAATGGCAAGCTCGACCGGCGAGGCGTTGCCGCAACCGGATGCGAGCTGTGCGAGCAGGCC
TATCGAGCGCCCGGTAGCGAGCTGGAGCAGCGATCGCAGCGATCTGGGCGGAGATCTGGGAGTGG

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AACGGGTCGGCCTGGACGACAACTTCTTCGAACTGGGCGGTCACTCATTGTTGCTGCTGATGCTCAA
GGAGCGGATCGGCGATACCTGCCAGGCTACGCTGAGCATCAGCCAACCTGATGACCCATGCCAGCGTC
GCGGAACAGGCGGCATGCATCGAGGGGCGAGGCGCGTGAGTCGTTGCTGGTGCCGCTCAACGGCAGGC
GCGAAGGTTCCGCGCTGTTTCATGTTCCATCCGAGTTTTCGGCTCTGTGCACTGTTACAAGACCCCTCGC
CATGGCGCTGCGGGATCGTCATCCGGTCAAGGGTGTGTCTGCCGTGCCCTGCTGGGCGCTGGTTCGC
GAGGTGCCGAGTGGGACGATATGGTTGCGGAATACGCCGAGCAATTGCTGCAGGAGCACCCCGAAG
GGGTTTTCAACCTGGCGGGATGGTCGCTCGGCGGCAACCTGGCGATGGATGTCGCGGCCCGGCTGGA
GCAGCGTGGGCGGACGGTGGCTTTCGTCGGCTGGATCGATGCACCGGCACCGGTGAGGGTCGAAGCG
TTCTGGAACGAGATCGGGCCGACGCCGAGGAGTCCCGAACCTATCCGTGGGCGAGATGCGGGTGG
AACTGCTCGGTGTCATGTTTCCGGAGCGGGCCGAGCATATCGAACGGGCGCTGGTCATCGATCTGCTC
CGCCACGACGGACGATGAGCAGCGCTGGACGAGGATGAGCGACTGGGCGGAAGCGGAGATCGGGCGCC
GAGTTCGCGACACTGCGCAGCGAAATCGCACAGAGCAACGAACCTGGAAGTGTCTCTGGGAGTTGAAAC
AGATCCTCGACGAGCGCCTGAAAGCGATGGATTACCCGCGTCTGACGGCGAAGGTGAGCCTCTGGTG
GGCCGCGCGCAGCACCAATGCCATCCAGCGGAGCGCGGTGGAGCGCTCGATGGCCGAGGCGATCGGG
GCTGAGCGTGTGCAACCGGTGCGGGTGTGGATACCCGGCAGCACAAGATCATCGACCACCCTGAGT
TTGTGCAGAGCTTCCGGGCGGCCCTGGAGCGTGCCGGGCGCTGA

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The VIR9 protein (SEQ ID NO:18) encoded by SEQ ID NO:17 is presented using the one-letter amino acid code in Table 11B.

Table 11B. Encoded VIR9 protein sequence (SEQ ID NO:18)

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MQALTEKVGSLSPQERKALAVLLKQQGVNLFETAPVFKRQDGEPLRLSYAQERQWFLWQLEPESA
AYHIPSVLRLRGRDLDALQRSFDSLVARHETLRTFRRLDGEARQETAAASMLPLDIVALGPLLE
EGALARQVETTIARPFDLERGPLLRVSLRLAEDDHVLLVQHHIVSDGWSMQVMVEELVQLYAA
YSRGLEVALPALPIQYADYALWQRSWMEAGEKERQLAYWTGLLGGEQPVLELPFDRPRPVRQSHR
GAQFILLELDIDLSQALRRVAQQEGATAFALLLASFQALLYRYSQADIRVGVPIANRNRVETERL
IGFFVNTQVLKADLDGRMGFDELLAQARQRALEAQAHQDLPFELVEALQPERSLSHNPLFQVLF
NYQSEARGNGQAFRFDLQMESVQFDSRTAQFDLTLDLTDEEQRFCAVFDYATDLFDASTVERLA
GHWNRLLRGIVANPRQRLGELPLLDAPERRQTLSEWNPAQRECAVQGTQQRFEEQARQRPQAVA
LILDEQRLSYGELNARANRLAHCLIARGVGADVPVGLALERSLDMVLVGLLAILKAGGAYLPLDPA
APEERLAHILDDSGVRLLLTQGHLLERLPRQAGVEVLAIIDGLVLVDGYAESDPLPTLSADNLAYVI
YTSGSTGKPKGTLLTHRNLRLFSATEAWFGFDERDVWTLFHSYAFDFSVWEIFGALLYGGCLVI
VPQWVSRSPEDFYRLLCREGVTVLNQTPSAFKQLMAVACADMATQPPALRYVIFGGEALDLQSL
RPFQRFQDRQPQLVNMYGITETTTHVHTYRVPVSEADLEGGLVSPIGGTIPDLWSYILDRDLNPVP
RGAVGELYIGRAGLARGYLRRPGLSATRFVNPFPFGGAGERLYRTGDLARFQADGNIEYIGRIDH
QVKVRGFRIELGEIEAALAGLAGVRDAVVLADHGVGGTQLVGYYVADSAEDAERLRESLRESLKR
HLPDYMVPAHMLLERMPLTVNGKLDRLQALPQPDASLSQAYRAPGSELEQRIAAIWSEILGVER
VGLDDNFFELGGHSLLATRVISRVREQQLDASLKALFERPVLEAFAQGLERTTDAVSTIPLADR
QQPLALSFAQERQWFLWQLEPESAAYHIPALRLRGRLDVDALQRSFDSLVARHETLRTFRLEG
GRSYQQVQPAVSVSIEREQFGEEGLIERIQAIIVQPFDLERGPLLRVNLQLAEDDHVLLVQHH
IVSDGWSMQVMVEELVQLYAAYSQGLDVLPALPIQYADYALWQRSWMEAGEKERQLAYWTGLLG
GEQPVLELPFDRPRPARQSHRGAQLGFELSRELVEAVRALAQREGASSFMLLLASFQALLYRYSQ
QADIRVGVPIANRNRVETERLIGFFVNTQVLKADLDGRMGFDELLAQARQRALEAQAHQDLPFEL
LVEALQPERNASHNPLFQVLFNHQSEIRSVTPEVQLEDLRLEGLAWDGQTAQFDLTLDIQEDENG
IWASFDYATDLFDASTVERLAGHWNRLLRGIVANPRQRLGELPLLDAPERRQTLSEWNPAQRECA
VQGTQQRFEEQARQRPQAVAILDEQRLSYGELNARANRLAHCLIARGVGADVPVGLALERSLD
MLVGLLAILKAGGAYLPLDPAPEERLAHILDDSGVRLLLTQGHLLERLPRQAGVEVLAIIDGLVL
DGYAESDPLPTLSADNLAYVIYTSGSTGKPKGTLLTHRNLRLFSATEAWFGFDERDVWTLFHSY
AFDFSVWEIFGALLYGGRLVIVPQWVSRSPEDFYRLLCREGVTVLNQTPSAFKQLMAVACADMA
TQQPALRYVIFGGEALDLQSLRPFQRFQDRQPQLVNMYGITETTTHVHTYRVPVSEADLKGGLVSP
IGGTIPDLWSYILDRDLNPVPRGAVGELYIGRAGLARGYLRRPGLSATRFVNPFPFGGAGERLYR
TGDLARFQADGNIEYIGRIDHQVKVRGFRIELGEIEAALAGLAGVRDAVVLADHGVGGTQLVGYY
VADSAEDAERLRESLRESLKRHLDPDYMVPAHMLLERMPLTVNGKLDRLQALPQPDASLSQAYRA
PGSELEQRIAAIWAEILGVERVGLDDNFFELGGHSLLLMLKERIGDTCQATLSISQLMTHASVA
EQACIEGQARESLLVPLNGRREGSPLFMFHPFSFGSVHCYKTLAMALDRHPVKGVVCRALLGAG
REVPEWDDMVAEYAEQLLQEHPEGVFNLAGWSLGGNLMAMDVAARLEQRGRQVAFVGVWDAPAPVR
VEAFWNEIGPTPEAVPNLSVGEMRVELLGVMPFPERAEHIERAWSSICSATTDDEQRWTRMSDWA
AEIGAFAFATLRSEIAQSNELEVSWELKQILDERLKAMDYPRLTAKVSLWAAARSTNAIQRSAVER
SMAEAIGAERVEPVRLDTRHDKIIDHPEFVQSFRALERAGR

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A *Pseudomonas* bacterial mutant (MUT10) was made by transposon insertion in a *P. aeruginosa* wild-type strain PT894. In the *Dictyostelium* growth assay, the mutated microorganism was less virulent compared to an isogenic bacterial strain. The nucleotide sequence immediately following the transposon insertion was cloned and identified as the gene encoding the RND multidrug efflux transporter MexD (mexD; PA4598). This gene encodes the VIR10 nucleic acid (SEQ ID NO:19) shown in Table 12A.

ATGTCCGAATTCTTCATCAAGCGGCCGAATCTCGCCTGGGTGGTGGCCCTGTTTCATCTCCCTGGCCG
GCCTGCTGGTCATTTCCAAATTCGGCTAGCGAGTACCCCAATGTCGCGCCGCCACAGATACCAT
CACCGCCACCTATCCCGGCGCCTCGGCGAAGGTGCTGGTGGACTCCGTACCAAGTGTGCTCGAGGAG
TCGCTGAACGGCGCCAAGGGCTGCTCTACTTTCGAGTCGACCAACAACACTCCAACGGCACCGCCGAGA
GAAAGCCGAGGCGCATGCCGAGGCGGTGCTGACCCAGGGCCTGCGAGGTGAGAGTGCAGAACCGCCGAA
GGTTTCTGCTGATCTATGCGTACGCTACAAGGAAGGCGCTCAGCGCAGCGACACCACCGCCCTCG
GCGACTACGCCGCGCGCAATATCAACAACGAGCTGCGGCGCTGCCGGGCGTCGGCAAGCTGCAAT
CTTCTCTTCCGAGGCGCCATGCGGGTCTGGATCGATCCGAGAAGCTGGTGGGCTTCGGCTCTCC
ATCGACGACGTGAGCAATGCCATCCGCGGGCAGAACGTGCGAGGTGCCGGCGCGCCTTCGGCAGCG
CACCGGGCAGTTCCCGCGAGGAGCTGACCGCGACCCTGGCGGTGAAGGGCACCTTGGACGATCCGCA
GGAGTTTCGGCCAGGTAGTGTCTGCGCGCAACGAGGACGGCTCGTGGTCCGGCTCGCCGATGTCGCG
CGCTTGGAACTCGGCAAGGAGAGTACAACATTTCTCGCAGTGAACGCGACGCCACCCTGCGGCG
GGGTATCCAGCTGTCGCCCGGGGCAACGCGATCCAGACCGCTACCTGGTGAACACGCGTCTCGC
CGAATGTCGGCGTTCTTCCCCGAGGACATGCAGTACAGCGTGCCTTACGACACCTCGCGCTTCGTC
GACGTGGCCATCGAGAAGGTGATCCACACCTGATCGAAGCGATGGTCTTGGTGTTCCTGGTGTATGT
TCCTGTTCTCGAAGCGCTCCGCTACACCTGATCCCGTCCATATGATACCATGTTTCGGCATGGTCTG
TACGCTGATGGTGTATGTACCTGCTGGGGTTCTCGTGAACATGATACCATGTTTCGGCATGGTCTG
GCGATCGGCATCTGGTGGACGACGCCATCGTGGTGGTGGAGAAGCTCGAGCGGATCATGGCGGAGG
AGGGGATTTCCCCGGCCGAGGCCACGGTCAAGGCGATGAAGCAGGTATCCGGCGCCATCGTCGCGAT
CACCTGGTGTCTTCGGCGGTGTTCTGCGGCTGGCTTTTCATGGCCGGTTCCGTGGGGGTGATCTAC
CAGCAGTTCTCGGTGCTGCGGTGCGGTCTGCATCTGTTCTTCGGCTTCTTCGCCCTGACCTTCACCC
CGCGCTGTCGCGCACGCTGCTCAAGCCATTTCCGGAAGGCGACCCAGAGAAGCGCGGCTTCTTCGG
CGCTTCAACCGTGGCTTCGCCCGCGTACCGAGCGCTATTTCGCTGCTCAACTCGAAGCTGGTGGCG
CGCGCCGACGCTTCATGCTGGTGTACGCCGGCTGGTGGCCATGCTCGGCTACTTCTACCTGCGCC
TGCCGGAAGCGTTTCGTGCGCGGCGGAAGACCTCGGCTACATGGTGGTGCAGCTGCAACTGCCGCTGG
CGCTTCGCGCTGCGCACCGGATGCCACCGCGGAGGAGCTCGAGCGCTTCTCAAGTCCCGCAGGGCG
GTGGCTTCGGTGTTCCTGATCTCGGGTTACGTTCTCCGGCCAGGCGGACAATGCCGCGCTGGCCT
TCCAACCTTCAAGGACTGGTCCGAGCGAGGCGCCGAGCAGTCCGGCGCGCCGAGATCGCCGCGCT
GAACGAGCATTTTCGCGCTGCGCGACGATGGCACGGTTCATGGCGGTGTCGCCGCCACCGATCAACGGT
CTGGGTAACCTCCGGCGGCTTCGCATTTGCGCCTGATGGACCGTAGCGGGGTGGCCGCGAAGCGCTGC
TCAAGGTTCGCGATACTCTTCTGGCGAGATCCAGACCAACCCGAAATTCCTTTACGCGATGATGGA
AGGACTGGCCGAAGCGCCGCAACTGCGCTGTGTGATCGACCGGGAAGGCCGTGCCCTGGGGGTG
AGCTTCGAGACCATCAGCGGCACGCTGTCCGCTGCCTTCGGCTCGGAGTGATCAACGACTTCACCA
ATGCGGGGCGCCAACAGCGGGTGGTGTATCCAGGCCGAACAGGGCAACCGGATGACCCCGGAAGCGT
GCTCGAGATATACGTGCCTAACGCTGCTGGCAACCTGGTACCGCTCAGCGCCTTCGTCAGCGTGAAA
TGGGAAGAGGACCGGTGCAATTTGGTGCCTATAACGGCTACCCGTCGATCCGATCGTGGTGACG
CCGCGCCCGGCTTCAGTACCGGCAAGCATGCGGGAATGGAGCGCCTGGCCTCGCAGCTGCCCGC
CGGCATCGGCTACGAGTGGACCGGCTGTCTTATCAGGAGAAGGCTCCGCGGGCAGGCCACGAGC
CTGTTCCGCCCTCGCCATCTGGTGGTGTTCCTGTTGCTGGTGGCGCTTCAGAGAGCTGGTGCATCC
CGCTGTGCGGTGATGCTGATCGTGCCGATCGGCGCCATCGGCGCGGTGCTCGCGGTGATGGTCAGCGG
TATGTCCAACGACGTGATTTCAAGGTCGGCTGATCACCATCATCGGCTTTTCGGCGAAGAACCGG
ATCCTCATCGTCAGTTTCGCAAGGAACCTGGGAGCAGGGGATAGCCTGCGCGACCGCGCATCG
AGGCCGCGCGCCTGCGCTTCCGGCGGATCATCATGACTTCATGGCGTTCATCTCGGCGTGATACC
CCTGGCCCTGGCCAGCGGTGCCGGCGCGGCGAGCCAGCGTCCGATCGGCACCGGAGTGCAGCGG
ATGCTCAGCGCCACCTTCTTCGGCGTGTGTTTCGTACCTATCTGTTTCGTCTGGCTGCTGCTGCTG

TGCGCAGCAAGCCGGCACCCATCGAACAGGCCGCTTCGGCCGGGGAGTGA

The VIR10 protein (SEQ ID NO:20) encoded by SEQ ID NO:19 is presented using the one-letter amino acid code in Table 12B.

Table 12B. Encoded VIR10 protein sequence (SEQ ID NO:20)

MSEFFIKRPNFAWVVALFISLAGLLVISKLPVAQYPNVAPPQITITATYPGASAKVLVDSVTSVL
EESLNGAKGLLYFESTNNSNGTAEIVVTFEPGTDPLAQVDVQNRLKKAEARMPQAVLTQGLQVE
QTSAGFLLIYALSYKEGAQRSDTTALGDYAARNINNELRRLPGVGKLOFFSSEAAMRVWIDPQKL
VGFGLSIDDVSNIRGQNVQVPAGAFGSAPGSSAQELTATLAVKGTLDQPQEFQGVVLRANEDGS
LVRLADVARELELGKESYNISSRLNGTPTVGGAIQLSPGANAIQTATLVKQRLAELSAFFPEDMQY
SVPYDTSRFVDVAIEKVIHTLIEAMVLVFLVMFLFLQNVRYTLIPSIIVVPVCLLGLTMLVMYLLGF
SVNMMTMFGMVLAIGILVDDAIVVVENVERIMAEEGISPAAETVKAMKQVSGAIVGITLVLSAVF
LPLAFMAGSVGVIIYQQFSVSLAVSILFSGFLALTFTPALCATLLKPIPEGHHEKRGFFGAFNRGF
ARVTERYSLLNSKLVARAGRFLVYAGLVAMLGYFYLRLEAFVPAEDLGVMVVDVQLPPGASRV
RTDATGEELERFLKSREAVASVFLISGFSFSGQGDNAALAFPTFKDWSEARGAEQSAAEIAALNE
HFALPDDGTVMAVSPPPINGLNSGGFALRLMDRSGVGREALLQARDTLLGEIQTNPKFLYAMME
GLAEAPQLRLIDREKARALGVSFETISGTLAAFGSEVINDFTNAGRQQRVVIQAEQGNRMTPE
SVLELYVPNAAGNLVPLSAFVSVKWEEGPVQLVRYNGYPSIRIVGDAAPGFSTGEAMAEMERLAS
QLPAGIGYEWTTGLSYQEKVSAGQATSLFALAILVVFLLLVALYESWSIPLSVMLIVPIGAIGAVL
AVMVGMSNDVYFKVGLITIIIGLSAKNAILIVEFAKELWEQGHSLRDAAEIAARLRFRPIIMTSM
AFILGVIPLALASGAGAASQRAIGTGVIIGMLSATFLGVLFVFPICFVWLLSLLRSKPAIEQAAS
AGE

MUT11

A *Pseudomonas* bacterial mutant (MUT11) was made by transposon insertion in a *P. aeruginosa* wild-type strain PT894. In the *Dictyostelium* growth assay, the mutated microorganism was less virulent compared to an isogenic bacterial strain. The nucleotide sequence immediately following the transposon insertion was cloned and identified as the gene encoding PA3721. This gene encodes the VIR11 nucleic acid (SEQ ID NO:21) shown in Table 13A.

Table 13A. VIR11 Nucleotide Sequence (SEQ ID NO:21)

ATGAACGATGCTTCTCCCCGCTGACCGAACCGCGGCAGGCAACGCCGCCGCGCCATGCTCGACGCCG
CTACCCAGGCCCTTCTCGAACACGGTTTCGAAGGCACCAACCTGGACATGGTGATAGAACGGGCGCG
TGTTTCACGGGGGACCCGTGTACAGCTCCTTCGGCGGCAAGGAGGGCCTGTTCGCCCGCGGTGATCGCC
CACATGATCGGGGAAATCTTCGACGACAGCGCCGATCAGCCGCGCCCCGCCGCCACGCTGAGCGCCA
CCCTCGAGCATTTTCGGCCGGCGCTTCTCACCAGCCTGCTCGATCCCCGCTGCCAGAGCCTCTATCG
CCTGGTGGTGCGGAATCCCCGCGGTTTCGGCGCATCGGCAAGTCCTTCTACGAGCAGGGGCGCGAG
CAGAGCTATCTGCTCAGCGAGCGACTGGCCGCGGTCGCTCCTCAGAGCAGGGGCGCGAG
ACGCGGTGGCCTGCCAGTTTCTCGAGATGCTCAAGGCCGACCTGTTCCTCAAGGCCCTCAGCGTGGC
CGACTTCCAGCCGACCATGGCGCTGCTGGAACCCGCTCAAGCTGTCGGTGGACATCATCGCCTGC
TACCTGGAACACCTGTGCGAGAGCCCCGCGCAGGGCTGA

The VIR11 protein (SEQ ID NO:22) encoded by SEQ ID NO:21 is presented using the one-letter amino acid code in Table 13B.

Table 13B. Encoded VIR11 protein sequence (SEQ ID NO:22)

MNDASPRLLTERGRQRRRAMLDAAATQAFLEHGFEGTTLDMVIERAGGSRGTLYSSFGGKEGLFAAV
IAHMIGEIFDDSDAQPRPAATLSATLEHFGRRLTSLLDPRCQSLYRLVVAESPRFPAIGKSFYE
QGPOQSYLLLSERLA AVAPHMDEETLYAVACQFLEMLKADLFLKALSVADFQPTMALLETRLKLS
VDIIACYLEHLSQSPAQG

5 MUT12

A *Pseudomonas* bacterial mutant (MUT12) was made by transposon insertion in a *P. aeruginosa* wild-type strain PT894. In the *Dictyostelium* growth assay, the mutated microorganism was less virulent compared to an isogenic bacterial strain. The nucleotide sequence immediately following the transposon insertion was cloned and identified as the gene encoding PA0596. This gene encodes the VIR12 nucleic acid (SEQ ID NO:23) shown in Table 14A.

Table 14A. VIR12 Nucleotide Sequence (SEQ ID NO:23)

ATGTCGTGATGATGCCCCGTTTCCAGCAGCTGAATTGCTGGTTGGACTCTTGTGTTGCCCGAGTTGTTCCG
TTGCCGAAGGTTGGGGGAAGTGCCCCCGCCGAAGTATCCCGGCCAGTAGCGACGCCAGCTTCCG
TCGTTATTTCCGCTGGCAGGGAGGGGACCGCAGCCTGGTGGTGATGGACGCGCCGCCGCCAGGAA
GACTGCCGACCGTTTCGTCAAGGTCGCCCGACTGCTCGCCGAGCCGGCGTGATGTGCCGAGGATTC
TCGCCCCAGGACCTGGAGAACGGTTTCCTGCTGCTCAGTGACCTGGGCGCGCAGACCTACCTCGACGT
GCTTCATCCCGGGAATGCCGACGAGCTGTTCTGAACCGGCCCTGGATGCGCTGATCGCCTTCCAGAAG
GTCGATGTGCCCGGTGTCTGCTGCTACGACGAAGCGGTGCTGCGCCGCGAGCTGCAGCTGTTC
CCGACTGGTACCTGGCCCGCCACCTCGGCGTGGAGCTGGAGGGCGAGACGCTGGCCCCGCTGGAAACG
GATCTGCGACCTGCTGGTACGCGAGCGCGCTGGAGCAACCGCGGGTGTTCGTCCATCGCGACTATATG
CCGCGCAATCTGATGCTCAGCGAGCCCCAACCCGGGCGTCTCGACTTCCAGGACGCCCTGCACGGCC
CGGTACCTACGATGTACCTGCCTGTACAAGGACGCTTTCGTGATTTGGCCGAGCCGCGCGTGCA
TGCCGCGCTGAACCGTTACTGGAAGAAGGCGACCTGGGCGCGCATCCCGCTGCCGCCAAGCTTCGAA
GACTTCTCCGTGCCAGCGACCTGATGGGCGTGACGCGCCACCTGAAGGTGATTGGCATCTTCGCCC
GTATCTGTACCCGCGACGGCAAGCCGCGCTACCTGGGTGACGTGCCGCGCTTCTTCCGTTATCTGGA
AACCGCCGTGGCGCGCGTCCCGAGCTGGCCGAAGTGGGCGAGCTGCTGGCCTCGCTGCCCGAGGGA
GCCGAGGCATGA

The VIR12 protein (SEQ ID NO:24) encoded by SEQ ID NO:23 is presented using the one-letter amino acid code in Table 14B.

Table 14B. Encoded VIR12 protein sequence (SEQ ID NO:24)

MSDDARFQQLNCWLDSCLPFLVAEGWGEVPPAELIPASSDASFRRYFRWQGGDRSLVMDAPPP
QEDCRPFVKVAGLLAGAGVHVPRILAQDLENGFLLLSDLGRQTYLDVLHPGNADELFEPAIDALI
AFQKVDVAGVLPAYDEAVLRRELQLFPDWYLARHLGVELEGETLARWKRICDLLVRSALAEQPRVF
VHRDYMPRNMLSEPNPGVLDFQDALHGPVTYDVTCLYKDAFVSWPEPRVHAALNRYWKKATWAG

IPLPPSFEDFLRASDLMGVQRHLKVIGIFARICHRDGPRLGDVPRFFRYLETAVARRPELAEL
GELLASLPQGAEA

MUT13

A *Pseudomonas* bacterial mutant (MUT13) was made by transposon insertion in a *P. aeruginosa* wild-type strain PT894. In the *Dictyostelium* growth assay, the mutated
5 microorganism was less virulent compared to an isogenic bacterial strain. The nucleotide sequence immediately following the transposon insertion was cloned and identified as the gene encoding PA5265. This gene encodes the VIR13 nucleic acid (SEQ ID NO:25) shown in Table 15A.

Table 15A. VIR13 Nucleotide Sequence (SEQ ID NO:25)

ATGAGCGGATTCCAGGACCAGAGTATCGACGAAGGCGTGCGCAAGCGCACCGCCTACCAGAACGATC
GGCGTGCACGACTGGCATTGAACGTCGAGCGACAGGACGGCGGTATCCTGCAGATTCCGGTGGCCAG
CGATATGCTCGGCCATGAGGAGCAGGAGCGTATCCAGCAGAACACCTTCTGGCTGTGATGCCGCTG
GTCCGCCTGCCAACGCTGGGCAAGGCCGGTTATGGCGACCAGCTGCCCGCCGGCGCTACCGCGGG
CGGGACGGATCTA C T G T T C C A G G A C G G C A A G T T G T G G C G C G A A C T G G A A T G T G A T G G C A A G G C A A
CCTGTTTCGAAGTCGATCTCCTGTCAGGGGCGCAGCCAGCGTGCGGACAAGCGTCCGGCCTTAGGCAAG
ACATAAGCGCTGATCCTGGTGGCGGTGCTGGTCAAGGGGCAAGTTCGTGATCCACGCTACACCATGG
CCTATAGCGAAACTCCCTGGCCTTGGTCGTACATCGACTGGCTGGAGGAGGACCCGACGCGGGTCAA
CCGGCGCTGCCAGCAGATGGCGTCCGCTTGGAACGCCCTCGGTGGCCAAACAGCACTGGAAAGCCTCC
ATCCATCAACCCGCGCTGGTCATTGATCATCACGCCAGGGTTTGGCGACCTCGCGACTTCAACGCTCG
AGAGCGCGCTGGAAGACCCGCGGGAATTCACACCTGAGTTCGCCGCTTTCGCGAAGAGTCGTGGT
GTGCCAGTTGCAGCGACGCCAGCAGGAATTTGGCGCCCTGCTGAAGCAGGCTCCGCCCTCTGCGCTA
CCTACTCTGGAAGCCGGAGAGGACGTACTGGAACCCCTCAAGCTGCGTGGCCATCCCAACCTCATCG
GGCTGATGCTCGACGACTCGCTGTTTCGCCCTTGGCCACGCTGCGGCGCAGGCGCGCCACTGCGCCGC
CTACTTGGCGACGCTCAATGCACGTGCTGCCGACCGTCCCAACGGACGCTATGCACAGGTGCTGAGC
AACATGCTCGACGGCCCGCTCGCCAAGCTCAGGGGCGAGGTGCGATCAGGCCGAAC TGGACGAGGCGA
TCTTCGCCGAGGAGCGACAGTCTTGCCGAATCCACCTGACGCAGCAGGTGCGATCTGGTTGCCCT
GCTGGAAGGCCCTTGCACCCGGTGTTCAGGACTGGACCCACAGTGCAGCAAGCCCTGCTGGAG
CCCTACAGCCTGATGAGCGAGGCACTGGCTGCGTGAACAGCTTCCGACCGCTGCGACGCACTGT
ACAGCGGTACCGCTTACCGGGCGCTGGCGGCACATGTCGAGCGGGTGGTCAGCACGCTTCTGCAAGG
AAGCCACCCGCTTGGCGCCATGCTCCTGGCCAAGGACGAAGGACAAC TCCCGAGCCGGTTTCGGCGC
CTGCAGGCGCTGCGCGATAGCCCGGGACGCCGGACCCCGATGCAATGGGCCCTCAGCACGCTGATGC
TGGGAGCCAGTCTGCTGGGCGAGGTGACAGCCAGCGCCGGCAAGAGCCTCGCCTACTTCTTCGG
CGACCTGCTGGACGTGTTCGGCGCCAGCGTAGTCGAGCAAC TCGGCCGGCTGTCCAGGGCGCCACC
CAGATCCAGCTCGACCGCTTGTTCGCACCGACCTTCAATACTCTGAGCGCCCTCTCGGTGAAGATGA
AAGGTATCCGCTGCTGCCCGACAGTCAGGTGCCGCTCGACATGGTTGTCTCGGCGTGC GCGGAGC
CGGCTGCGCAACGGTCTGACCGAGGTGAGCGCCAGGAGCTGAGGCGCAAGAGCTATCGGCGCGCC
ATCGTTCAGGACGGTGCCGGCAATCCCTGGCCGGCACCAGTCCCGCGACACCGGCATGAGTCGCG
CCAACCTGCGCAACGTCATGGTGGTGGCGGTACCCAAAGGATCACCCGGACCTGCTTGCTTACACGAA
ATTCCTACGCACTTAGGCACGTTGACCCAGGTGATGGAGAACA CTGCGATCGTGCCGACGATGATG
CTGGGGTTTGC GATT TATAACTTGAATGTGAGGTGCAAGCATA CAGTGGCTTTGTAGACAGTGGAG
AAAAGCACAGAGGACGATCGGGGCTGTCGGTGCAGTAATCGATT TAAACAGCCGCTGGAGGAAGCCA
TGCAAAGCTGCTTTTTCGGACCATCTACTGCAAGTATCTAGAAACCCACGTATATCGGTAGCCCAA
ATATCCCTTCGATGGGCCAGGAATCTAGAACTTCAAGAGTATCTAGAAACCCACGTATATCGGTAGCCCAA
GGCTTGGTGGCGCAGCCACACTATTGGTGCAGGCATCAGTGTATGGGATGGCTACCGAGCTTTGAG
GCAGGGAGATAGCGATGCGGCTGCGGCTACCGTGTGGCCGCACTGGGTGGGGGCTTTGGGGTGCC
TAGCTCTAGGATGGATAGTAAACCTTATGCTTTGCTGGCTGGTGGCTTTTGGCGATCGGAGGCA
CTGTTGCTCGCTAATCTACTGACTGACAGCGATGCGGAAACCATCGTAAAGAAAGGCCCTTCGGCCG
GCAATTCGCCGAGGCTGGCCTGCTCGATTGCTGCTGAGTGGGCCAGGACGAGCTTCGCCCATCTGAA
GACCCGCAACGGCTATCGCCAATTGCTGGGAGTCTCGGCCATCCGCGGGTCTTTGTCCATCGCC
TGGAAGACTGGCGCAATTTGGCGCCGGCGGCGCATCGATCTGTCTGCAAGGAAGCGGAACGGGGTTCG
CCAAGCGGTACGCCACTGCGCTATCCTGCATCGACCCAAAGTTGCAAGCGCTGGAGGCAACGAT

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TGGGCCGTGGTGCTGAGTTCCCGCTCCTGGCCATGTTTCGAGAATGGCCAGAAGGCGTTCCGCCTGG
TGGCCCAGGAGTTTCTCAGCAGCTTGCCGATCGATCCGGGCACCCTGTTTCGGCGTCAAGCGCTACCA
TCGGGTCCCCGCGGGCCCCGCAAGCTCGAAGCCTTGCCGTTGGATGCTGCCAGCGTGCTCTATGTG
CTGCCGGCCAGCCTGCCGATTCCGCAGTTGTCTCCTCGGGCCGCTATAGCATGCGCATGACCCAGG
GTTTGAAGATCAGCGCACAGTTCGAACTCAATGCCGACCAGCCTGAGCAGCGGCTTGTCTGCCTCA
ACCCAGCCCGAAGAGTTGGAGTGCATTACATCCGCCAATCGGTACCTTCCCCCGGACGACTTGGGC
CCCCATGCTGCGCCACCTTATTGGTTGATAGAGAACAGTGAGTTCAACGTATGA

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The VIR13 protein (SEQ ID NO:26) encoded by SEQ ID NO:25 is presented using the one-letter amino acid code in Table 15B.

Table 15B. Encoded VIR13 protein sequence (SEQ ID NO:26)

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MSGFQDQSIDEGVRKRTAYQNDRRARLALNVERQDGGILQIPVASDMLGHEEHERIQNTFLAVM
PLVRLPTLGKAGYGDQLPAGALPRAGRIYLFQDGKLWRELECDGKGNLFVDDLQGRSQRADKRP
ALGKTQALILVPVLVKGFVPIPRYT MAYSETPWPSYIDWLEEDPQRVNRRCCQMASAWNASVAN
QHWKASIHQFALVIDHHAQGLRPRDFNVE SALEDPAEFTPEFAAFREESLVCQLQRRQQLAPLL
KQAPPSALPTLEAGEDVLETLKLRGHPNLI GLMLDDSLFALRHAAAQARHCAAYLRSLNALLPHR
PNGRYAQVLSNMLDGPLAKLRGEVDQAE LDEAIFAEERQSCRHLTQQVEHLVALLEGPLHPVLQ
DWT HQDEALLEPYSLMSEAL AALNQLPDRCDALYSGTAYRALAAHVERVVSTVLQASHPLGAML
LAKDEGQLPEPVRRLQALRDSRPTPD PDAMGLSTMLGASLLGEVDQPSAGKSLAYFLGDLLDVF
GASVVEQLGRLSQGATQIQLDRLFAPTFNTLSALSVKMKGIRLLPDSQVPLDMVVVGVRGAGLRN
GLTEVERQELRRKSYRRAIVQDGAGNPLAGTSPRDTGMSRANLRNMVVAVPKDHPDLLAYTKFR
TQLGTLTQVMENRIVPTMMLGFAIYNLNVQVQAYS GFVDSGEKHRGTIGAVGAVIDLTAAGGSH
AKLLFGPSTAKYLETPRISVAQISPRWARNLEVQTGSPKLGLLRGLGGAATLFGAGISVWDGYRA
LRQGDSDAAAAAYGVAAVGGGLWGAYVLGWIVNYPYALLAGAVLAIGGTVVANLLTSDAETIVKKG
PFGRQFAEAGLLDSL MGQDQRF AHLKDPQTAYRQLLGVLGHPRVFVHRLEDWRKLAPAAHRSVLQ
EAERGRQAVSR TALSCIDPKLQALEANDWAVVLS SPLLAMFENGQKAFRLVAQEFLSSLPIDPGT
LFGVKRYHRVPAGPAKLEALPLDAASVLYVLPASLP IQLSPRARYSMRMTQGLKISAQFELNAD
QPEQRLVLPQPSPKSWSAFTSANRYLPDDDLGPHAAPPYWLIENSEFNV

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5

MUT14

A *Pseudomonas* bacterial mutant (MUT14) was made by transposon insertion in a *P. aeruginosa* wild-type strain PT894. In the *Dictyostelium* growth assay, the mutated microorganism was less virulent compared to an isogenic bacterial strain. The nucleotide sequence immediately following the transposon insertion was cloned and identified as the gene encoding pyochelin biosynthetic protein pchC (PA4229). This gene encodes the VIR14 nucleic acid (SEQ ID NO:27) shown in Table 16A.

Table 16A. VIR14 Nucleotide Sequence (SEQ ID NO:27)

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ATGAGCGCCGCTGGGTCCGGCCGTTCCGCCTGACGCCGATGCCGCGCCTGCGCCTGGCTTGCTTCC
CCCATGCAGGCGGCAGCGCCAGCTTCTTCCGTAGCTGGAGCGAACGCCGTGCCGCCAGACATCGACCT
GCTTGCCCTGCAGTACCGGGTCGCGAGGACCGCTTCAACGAGGCGCCGGCCACCCGCCCTGGAGGAC
CTCGCCGACGGCGCCGCCCTCGCCCTGCGCGATTTGCGCGACGCGCCCTGGCGCTGTTGGGCCACA
GTCTCGGCGCGGCGCTGGCCTACGAAACCGCCCTGCGCCTGGAAAGCGCCGGCGCGCCGCTGCGCCA
CCTGTTGCTCTCCGCCATCCGGCACCGCACCGGCAACGCGGCGGCGCGCTTGCACCGGGCGACGAG
GCGGCGCTGCTGGAGGACGTCCGCCGCCAGGGTGGCGCCAGCGAGCTACTCGAGGACGCCGACCTGC
GCGCGCTGTTCTTCCGTGCCGATCCTGCGCGCCGACTACCAGGCGATCGAGACCTACCGACGGGCGCAGCC

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CATCGCCCTGGCCTGCGCCCTCGACGTCCTCCTCGGCGAGCAGCAGGAAAGTCAGCGCCGCCGAG
GCGCAGGCCTGGAGCGACGCCAGCCGACTCCCGCCAGGCTGCGGCGCTTTCCTGGCGGCCACTTCT
ACCTGAGCGAGGGGCGCGACGCGGTGATCGAGCACCTGCTGCGCCGCTCGCACATCCCGACGCCCT
TTCCCGAGAGGTTGCATGA

The VIR14 protein (SEQ ID NO:28) encoded by SEQ ID NO:27 is presented using the one-letter amino acid code in Table 16B.

Table 16B. Encoded VIR14 protein sequence (SEQ ID NO:28)

MSAAWVRPFRLLTPMPRLRLACFPHAGGSASFRRSWSERLPPDIDLLALQYPGREDRFNEAPATRLLEDL
ADGAALALRDFADAPLALFGHSLGAALAYETALRLESAGAPLRHLFVSAHPAPHRQRGGALHRGDEAA
LLEDVRRQGGASELLEDADLRLFLPILRADYQAIETYRRAQPIALACALDVLGHEDEEVSAEAQA
WSDASRTPARLRFPGGHFYLSEGRDAVIEHLLRLAHPDALREVA

MUT15

A *Pseudomonas* bacterial mutant (MUT15) was made by transposon insertion in a *P. aeruginosa* wild-type strain PT894. In the *Dictyostelium* growth assay, the mutated microorganism was less virulent compared to an isogenic bacterial strain. The nucleotide sequence immediately following the transposon insertion was cloned and identified as the gene encoding dihydroaeruginic acid synthetase pchE (PA4226). This gene encodes the VIR15 nucleic acid (SEQ ID NO:29) shown in Table 17A.

Table 17A. VIR15 Nucleotide Sequence (SEQ ID NO:29)

ATGGATCTGCCCCCGATTCCCGTACCGCCCTGCGCGACTGGCTGACCGAGCAGCTCGCCGACCTGCG
TCGGCGAACCGCTTGCTGACGTGCGCGCCCTGGCGGACGACGACGACCTGCTGGGCTGCGGCCCTCGA
CTCGATCCGCCTGATGTACCTGCAGGAACGCCCTGCGCGCGCGTGGCTCGACGCTGGACTTCGCCCGAG
TTGGCGCAGCGCCCCTGCTGGGGGGCTGGCTCGACCTGCTGGCTGCGCGGACCGGCTGTCCGCC
CGGCAACGGTCGCGCTGCCGACGGCGCAGGATCGCGATCAGCCGTTTCGAGCTGTCTTCCTGTCAGCA
GGCTTACTGGCTGGGACGTGGCGCCGGCAGGTGCTGGGCAACGTCAGCTGCCATGCCCTTCTGGAA
TTCCGCACGCGGGATGTGACCCGCGAGCGCTGGCGCGCGGCGGAGTGGCTGCGTCAACGCCACC
CGATGTTGCGGGCGCGCTTCTTCGACGGTCGCCAGCAGATCCTTCCGACGCGCGCGCTGTCTGCTT
CGACCTGCAGGACTGGCGCACCTTACAGGTGGACGAGGCCGAGCGCGACTGGCAGGCGCTGCGCGAC
TGGCGCGCCCATGAATGCCCTGGCGGTGGAGCGCGCCAGGTGTTCTGCTCGGGCTGGTGCATGC
CGGCGGCGAGGATCGCTCTGGCTGAGTCTCGACCTGCTTGGCGCCGATGTGAAAGCCTGCGCCT
GCTGCTGGCCGAACCTGGGCGTTGCCCTACCTGGCGCCGGAGCGCCTGGCGGAGCCGCCCGGCGCTGCAT
TTCGCCGACTACCTGGCGCACCGTGCGGCGCAACCGCGCCGAGGCCGCGGCGCGGGCCCGCGACTAC
GGCTGGAACGCCTGCCGCGCTTGCCGACGCGCGCGCCCTGCCGTTGGCTGCGCGCCGGAAGCAT
CCGCCAGCCGCGCACCCGGCGCCTGGCATTCCAGCTTTCGCCCGCGCAGAGCCGCGCGCTGGAGCGT
CTTGCCGCGCAGCATGGCGTGACCTTGTCCAGCGTGTTCGGCTGCGCCTTTCGCGCTGGTCTTGGCG
GCTGGAGCGAAAGCGCGGAATTTCTCCTCAACGTGCCGTTGTTTCGATCGGCATGCCGACGACCCGCG
TATCGGCGAGGTGATCGCCGACTTCACCACCCTGTTGCTGCTGAGTGGCGGATGCAGGCCGGGTG
TCCTTCGCCGAGGCGGTGAAGAGCTTCCAGCGCAACCTCCACGGAGCCATCGACCACGCCGCATTCC
CCGCCCTGGAGGTGCTCCGCGAGGCGCGCCGGCAGGGCCAGCCACGCTCGGCGCCGCTGGTGTTCGC
CAGCAACCTGGGCGAGGAGGCTTCGTCCCGCGGCGCTTCCGCGACGCTTTCGGCGATCTCCACGAC
ATGCTCTCGCAGACCCCGCAGGTCTGGCTCGACACCAAGCTTACCGGGTGGGCGACGGTATCCTGC
TGGCCTGGGATAGCGTCTGCGCCTGTTCCCGAAGGTCTGCCGAAACCATGTTTCAAGCCTACGT
GGGCTGCTCCAGCGTCTTGCGACAGCGCTGGGGCGAGCCCGCGATCTGCCGTTGCCCTGGGCG

CAGCAGGCGCGCCGGGCTGCTCAACGGCCAGCCGGCATGCGCCACGGCGCGCACCTGCATCGCG
 ACTTCTTCTTTCGCGCCGCCGAGGCGCCGGATGCGGACGCGCTGCTCTATCGCGACCAACGTGTAC
 CCGCGGCGAACTGGCCGAGCGTGCCTGCGCATCGCCGGCGGCTGCGCGAAGCCGGGGTGCGCCCT
 GCGGACGCGGTGAGGTACGCTGCGCGCGGACCGCAGCAGGTGCGGCGGTATTCGGCGTGTCTCG
 CCGCAGGCGCCTGCTACGTGCCGTGGACATCGACCAGCCGCCCGCACGGCGGCGCTGATCGAAGA
 GCGCGCGGGGTATGCCTGGCGATACCGAGGAGGACGATCCGCAGGCCCTGCGCGCGCGCTGATCGAAGA
 GTCCAGCGCCTGCTGCGCGGCGCGGCTGGCCGCCCGCTGCGCGCTGGCGCGCGAGGCGAGTGCCT
 ATGTGATCTACACCTCGGGCTCCACCGGGGTGCCAAGGGCGTCAGGTCAGCCACGCGCGGCGAT
 CAATACCATCGACGCGCTGCTCGACCTGCTGCGGGTGAACGCATCGGATCGCTTGTGCGCGGTCTCC
 GCGCTGGACTTCGATCTGTGCGTCTTCGACCTGTTGCGCGGCTCGGCGCGGCTGCCAGCCTGGTCC
 TGCCGGCCAGGAACAGGCGCGGATGCCGTGCCGTGGCGGGAGGCTATCCAGCGGCATGCGGTGAG
 CCTGTGGAACTCGGCGCGGCTTGTGAGATGGCCCTCAGCCTGCCGGCGAGCCAGGCGGCTAT
 CGCAGTCTGCGGGCGGTGCTGCTGTCCGGCGACTGGGTGGCCCTGGACCTGCCCGCGGCTGCGCC
 CACGTTGTGCCGAAGGCTGCCGCCCTGCATGTGCTGGGTGGCGCTACCGAAGCGGGCATTTGCGGGA
 CCTGCAGAGCGTCGATACGGTGGCGCGCACTGGCGTTTCGATTCCCTACGCGCGGCGCATTTGCGGGA
 CAGGCCCTACCGGGTGGTTCGACACCCACGGCGCGACGTGCCGGACCTGGTGGTTCGCGAGCTGTGGA
 TCGCGCGGCGCGAGCCTGGCCCGCGGCTATCGCAACGATCCCGAATCAGCGCGCGCGCTTTCGTCCA
 CGATGCCCAGGGCGCTGGTATCGCACCGGCGATCGCGGTTCGCTTACGGCGGCGAGCTGTGGA
 TTCTTCGGTTCGGTTCGACAGGCTGAAAGTGC CGCGGCGAGCGCATCGAGTTGGCGAGGTGGAGG
 CCGCGCTGTGCGCCAGGCTGGCGTGGAGAGCGCTGCGCGCGCGGTGCTCGGCGGTGGCGTGGCGAG
 CCTCGGCGCGGTGCTGGTACCGCGCTGGCGCCACGGGCGGAAGGCTCCATGGATCTACCGCGCGCA
 CAGCCCTTCGCGCGGCTGGCAGAGGCGAGGCGGTACTACCGGGAAATCCTCGGCGCGCTGCTGG
 AGGCGCGCTGGAGCTAGACGACGGTTTGGCGCGCGCTGGCTGGACTGGCTAGCGGACTCCGCCCG
 CAGCGCGCTGCGCTCGCTCGACGAGGCGTTGCGCGGCTCGGCTGGCAGGCGCGCGGCTGACCGCG
 ATGGGCAACGCTCTGCGCGGCTGCTCGCGCGCGAAGCGCGCGCGGCGCGCTGCTCCTCGATCCCT
 GGCTGGCGCGCGAGGCGGTGGCGCGCGCTGCGGACGGCGCGAGGCGCTGGCGCGCGCTGCTCCTCGATCCCT
 AGCGCTGCGGACGCGCGCTGCGCGCGAAGCGCTGCGGAGGCGCGCGAGGCGCTGGCGCGCGCTGCTCGA
 TGGCTCGACAGGCGATGGCTCGCTGTTGCGCGCGAGGCGTGAAGTACCTCTTCGAACGCAGCC
 GCGTCTCTCGACGCGCGCGCCACCGCTTGGCGGAACGGATCGTGGTGCAGGCGCTGGACGACCG
 CCTGCTACCTGCCGAGCAGCTCGGTCGCTACGACCGGCTGATCAGCTTCGCGCGCTGCACGCGCTAC
 GAGGCGAGCGCGAAGGCTGGCGCTGGCGCGCGCTGCTGCGCGCGCAGGCGCGCTGTTGCTGG
 TGGACCTGCTATGCGAGTCCGCACTGGCGCTGCTCGGTGCGGCTGCTGCGCGCGCAGGCGCGCTGTTGCTGG
 CCTGGCGGAGCTGCGGAGCCTGTTGGCGGATCTCGCGCTGCGGCGCTGCTGCGCGCGCAGGCGCGCTGTTGCTGG
 CGCAGCGAGCGGATCGCCCTGGTTCGAGGCGCTGGCACCAGGACTCGGCGCTGCGCGCGCTGCTGCTGG
 AGGCGCGCTGGAGCAACGCTGCCCCAGGCGATGCGGCGCGAAGCGCTGTGGTGCCTGCCAAGCCT
 GCCGTTGAACGCGCAATGGCAAGGTGATCGTCCGCGCTGGCGGAGAGCATGACCCGCGCACTCGGC
 GAGTGTGCTACGAGCCCTCGGCGGAGGAGCGCTGGAAGCCCATGAGCAAGCGCTGGCGGAGTGTGCT
 GGAAGCGGTTCTCAAACGCGCGGTGCGTCTGCGGAGGCGAGCTTCTTCAGCCTCGGCGCGAGTGTGCT
 CCTGCTGGCGAGCCGCTGCTGGCGCGCATACGTGAGCGTTTCGGCGTACGCTGGCGATGGCGAG
 TTCTATCGCCAGCCGACCTGGCGGCTTTCGCCCGCACTTGCAGGTGCAGACCGTGCAGAAATCGAGG
 AAACCAACTGGAAGAGGCGGTGCTATGA

The VIR15 protein (SEQ ID NO:30) encoded by SEQ ID NO:29 is presented using the one-letter amino acid code in Table 17B.

Table 17B. Encoded VIR15 protein sequence (SEQ ID NO:30)

MDLPDSRTALRDWLTEQLADLLGEPLADVRLADDDLLGCLDSIRLMYLQERLRARGSTLDFAQL
 AQRPLGAWLDDLACADRLSAPATVALPTAQDRDQPFELSSVQQAYWLGRGAGEVLGNVSCHAFLEFR
 TRDVPQRLAAAAECVRQHPMLRARFLDGRQILPTPPLSCFDLQDWRTLQVDEAERDWAQALRDWRA
 HECLAVERGQVFLGLVRMPGGEDRLWLSDLADVESLRLLLAELGVAYLAPERLAEPALHFADY
 LAHRAAQRRAAARADYWLRLPRLPDAPALPLACAPESIRQPRTRRLAFQLSAGESRRLERLAAQH
 GVTLSVFGCAFALVLARWSESAEFLNLNPLFDRHADDPRIGEVIADFTTLLLECRMQAGVSFAEAV
 KSFQRLHGAIDHAAFPALEVLREARRQGQPRSAFVVFASNLGEEGFVPAAFRDAFGDLHMLDLSQTPQ
 VWLDHQLYRVGDGILLAWDSVVGLEFPEGLPETMFEAYVGLLQRLCDSAWGQPADLPLFWAQQARRALL
 NGQPACATARTLHRDFFLRAAEAPDADALLYRDQRVTRGELAERLRIAGGLREAGVRPGDAVEVSLP
 RGPQQVAAVFGVLAAGACYVPLDIDQPPARRRLIEEAAGVCLAITEEDDPQALPRLDVQRLLRGPAL
 AAPVPLAPQASAYVIYTSGSTGVPGKVEVSHAAINTIDALLDLRVNASDRLLAVSALDFDLVDFDL
 FGGLGAGASLVLPAQEQARDAAWAEAIQRHAVSLWNSAPALLEMALSLPASQADYRSLRAVLLSGDW
 VALDLPGRLRPRCAEGCRLHVLGGATEAGIWSNLQSVDTVPPHWRSPYGRPLPGQAYRVVDTHGRDV

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PDLVVGELWIGGASLARGYRNDPELSARRFVHDAQGRWYRTGDRGRYWGDGTFLEFLGRVDQOVKVRGO
RIELGEVEAALCAQAGVESACAAVLGGGVASLGAIVLPRLAPRAEGSMDLPAAQPFAGLAEEAEAVLTR
EILGALLEAPLELDDGLRRRWLDWLADSAASALPSLDEALRRLGWQAAGLTAMGNALRGLLAGEQAPA
ALLLDPWLAPQAVARLPDGREALARLLEALPTPAAGERLRVAVLDTRAGLWLDQGMASLLRPGLELT
LFERSRVLLDAAATRLPERIVVQALDDGLLPAEHLGRYDRVISFAALHAYEASREGLALAAALLRPQG
RLLLVDLLCESPLALLGAALLDDRPLRLAELPSLLADLAAAGLAPRCLWRSERIALVEALAPGLGLDA
AALQAGLEQRLPQAMRPERLWCLPSLPLNGNGKVDRRRLAESMTRALGECRHEPSAEEPLEAHEQALA
ECWEAVLKRPRRREASFFSLGGDSLALATRLLAGIRERFGVRLGMADFYRQPTLAGLARHLQVQTVEI
EETQLEEGVL

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MUT16

A *Pseudomonas* bacterial mutant (MUT16) was made by transposon insertion in a *P. aeruginosa* wild-type strain PT894. In the *Dictyostelium* growth assay, the mutated microorganism was less virulent compared to an isogenic bacterial strain. The nucleotide sequence immediately following the transposon insertion was cloned and identified as the gene encoding pyochelin synthetase *pchF* (PA4225). This gene encodes the VIR16 nucleic acid (SEQ ID NO:31) shown in Table 18A.

Table 18A. VIR16 Nucleotide Sequence (SEQ ID NO:31)

```

ATGAGCCTCGGCGAAGTGC'TGGAAACCTGCCGCAGCCGGCGCATCGAACTCTGGAGCGAGGCGGGCC
GCCTGCGCTATCGCGCCCCCAGGGTGCCCTCGACGCCGGCCTCGCCGAGCGCCTGCGGGCCGAGCG
CGAGGCCCTGC'TGGAACACCTGGAAGGCGGGCCCTGGCTGGCGCGCCGAACCCGACATGGCCACCAG
CGCT'TCCCGCTGACCCCGGTGCAGGCCGCC'TACGTGCTGGGCCGCCAGGCGGCC'TTCGACTACGGCG
GTAACGCC'TGCCAGCTGTACGCCGAGTACGACTGGCCGGCCGACACCCGATCCGGCGCGCCTGGAGGC
GGCCTGGAACGCGCATGGTTCGAGCGCCACCCGATGCTGCGCGCGGTGATCGAGGACAACGCC'TGGCAG
CGCGTGCTGCCCGAGGTGCCCTGGCAGCGGCTGACCGTGCAATGCC'TGCGCGGGCTCGACGAGGCCG
CTTTCCAGGCGCACCTGGAGCGGGTCCGCGAACGCCCTCGACCACGCC'TGCGCGGGCTCGACGAGGCCG
GCCGGTCT'TGCGCCCCGAGCTGAGTATCGGCCGGGATGCC'TGCGTACTGCACTGCTCGGTGGATTTC
ACCTTGGTTCGACTACGCCAGCCTGCAAT'TGCTGCTTGGCGAATGGCGCCGCCGCTATCTCGATCCGC
AATGGACGGCGGAACCGCTGGAGGCGACCT'TCCGCGACTATGTGCGCGTCGAGCAGCGCCGACGCCA
GTCGCCAGCCTGGCAGCGCGACCGCGACTTGGTGGCTGGCGCGCTCTCGACGCGCTACCGGGGCGTCCC
GACCTGCCCGCTGCGGGTGCAGCCGGACACCCGGTCCACGCGCTTCCGGCACTTCCACGCGCGCCTCG
ACGAGGCCGCGCTGGCAGGCGCTCGGCGCGCGCGCGCGCGGAACACGGCCTGAGCGCTGCCGGCGTGGC
CTTGGCGGCCCTTTCGCCGAGACCATCGGTGCTGGAGCCAGGCAACCGCGCTTCTGTCTCAACCTGACG
GTACTCAACCGGCGCGCTGCAATCCGAGCTGGCGCAGGTGCTCGGTGACTTCACCGCGCTCAGCC
TGCTGGCAGTGGACAGCCGCCACGGCGACAGTTCGTCGAGCGTGCCCGACGCATCGGCGAGCAGAT
GTTTCGACGACCTCGACCACCCGACCTTCAGCGGCGTGCAGCTGCTGCGCGAAGTGGCGCGCGCGCT
GGTCGCGGCGCGGATCTGATGCCGCTGGTGTTCACCACTGGCATCGGCAGCGTGCAGCGCCTGCTCG
GCGATGGCGAGGCGCGCGCGGCCACGCTACATGATCAGCCAGACCCCGAGGTCTGGCTGGACTG
CCAGGTACCCGACGTTTCGGCGCGCTGGAGATCGGCTGGGACGTACGCCCTCGGGTTGTTCGCCGAG
GGCCAGGCGGAAGCCATGTTTCGACGACTTCGTCGGGCTGCTCCGGCGCCTGGCGCAGAGCCGCGCG
CCTGGACCGACGGCGATGCCACGGAACCCGTCGAGGCGCGCGCGCAGGCGTTGCCCGGTAGTGCCCG
GAGCATCGCCCGCGGTTTCGCCGAGCGTGCCCTGCTGACCCCGACGCCACGGCGATCCACGATGCC
GCCGGCAGCTACAGCTACCGCCAGGTGCGCCAGCACGCCAGCGCCCTGCGCCGCGCTCTTGGAGCGC
ACGGCGCGGGCGCTGGCCGCGGGTTCGCGGTGCTGCGGAAAAGCGCCGCGCAATTTGGTTCGCGGT
GATCGGCATCTTCCAGGCGGGCGCGCCTATGTGCTGGCGGTTGGACATCCGCCAGCTCCGCTGCGGCGC
CAGGCGATCTCGCCAGCGCCGAAGTGGTTCGCGCTGGTTCGCTGGAAAAGCGATGTCCCGAGCGTCG
GCTGCGCCTGCGTGGCCATCGACCGGCTGGCCGCCGACAGCGCCTGGCCGCCACCGCCCGCGCGGA
GTTGGCGGCGGACGACCTCGCCTACGTGATCTACACCTCCGGCTCCACCGGCACGCCAAAGGGCGTG
ATGCTCAGCCATGCGCGGCTGAGCAACACGCTGCTCGACATCAACCAGCGCTACGGCGTTCGACGCCA
ACGACCGCTCTCGGCTCGCCGAGCTGAGCTTTCGACCTCTCGGTCTACGACTTCTTGGCGGCCAC
CGCGCGGGGGCCAGGTGGTCTCCCGGACCCGGCGCGCGGCGAGCGATCCATCGCACTGGGCGGAA
CTGCTGGAACGCCACGCCATCACCTGTGGAACCTCGGTGCCGGCCCAAGGCCAGATGCTCATCGATT
ACCTGGAGAGCGAGCCGCAACGTCACCTGCCGGGACCGCGCTGCGTGCTCTGGTCCGGTGAAGTGGAT

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TCCGGTCAGCCTGCCGACCCGCTGGTGGCGGCGCTGGCCGGACAGCGCGCTGTTTCAGCCTGGGCGGC
GCCACCGAGGCGGCGATCTGGTCGATCGAGCAGCCGATCCGCCCGCAGCACACCGAGCTGGCCAGCA
TCCCTTATGGCCGTGCCCTGCGCGGGCAGAGCGTGGAAGTCCCTGGATGCCCCGCGGGCGGCGCTGCC
GCCGGGCGTGCGCGGCGAGATCCATATCGGCGGGGTGGGCCCTGGCGCTCGGCTACGCCGGCGATCCG
CAGCGCACCGCCGAACGCTTCGTCCGTCACCCCGATGGCCGTCGCCCTGTATCGCACCGGCGACCTCG
GCCGCTACCTGGCCGACGGCAGCATCGAGTTCCCTCGGCCGCGAGGACGACCAGGTGAAGATTTCGCGG
CCACCGCATCGAACTGGCCGAACCTGGACGCGCGCGCTGTGCGCTCATCCGACAGGTCAACCTGGCGGCC
ACCGTGGTGCTCGGCGAGACCCACGAGCGCAGCCTGGCCAGCTTCGTACCCCTGCATGCGCCGGTGG
AGGCTGGCGAGGATCCGCGTACGGCGCTCGACGCGGTGCGCCAGCGGGCGGCCAGGCCTTGCGCCG
CGACTGGGGCAGCGAGGAGGGCATCGCCGCGGCGGTGGCCGCACTCGACCGTGCCCTGCCTCGCCTCG
TTGGCCGCTGGCTGGCCGGCAGCGGTCTGTTCGCCAGTGCGACGCCGCTGGACTTAGCCACCCTGT
GCCAGCGCCTGGGTATCGCCGAGGCGCGCCAGCGCCTGCTGCGCCACTGGTTGCGCCAACTGGAGGA
GGGCGGCTACCTGCGCGCCGAGGGCGAGGGCTGGCTGGGCTGCGCCGAGCGTCCCGCGCAGAGTCCG
GAGGACGCTGGACGGCGTTCGCCGGCTGCGCGCCGGCGGCGCTCTGGCCGGCCGAGCTGGTTCGCT
ACCTGCGTGACAGCGCGCAATCCCTCGGCGAGCAACTGGCCGGGCGGATCAGCCCGGCGGCGCTGAT
GTTCCGCGAGGGCTCGGCGCGCATCGCCGAGGCCATGTACAGCCAGGGCTGCATGCCAGGCGCTG
CACAGGCCATGGCCGAGGCCATCGCCGCCATCGTCGAGCGCCAGCCGCAACGGCGCTGGCGCCTGC
TGGAGCTTGGCGCCGGCACCGCCGCCGCCAGCCGACGGTGATCGCCCGTTGGCGCCGCTGGTGCA
GCGAGGGGCGGAGGTGGACTACCTGTTTACCAGCTTTCAGCTACTTCCCTCGCCGCGCCCGCGAG
CGCTTCGCCGACCGCCGTGGGTACGCTTCGCCCGCTTCGACATGAACGGCGATCTTCGACACAGG
CGGTGGCGCCGCACTCGGTGGATATCTGCTCAGCTCCGGGGCTTGAACAACGCGCTGGACACCC
GGCGCTGCTGGCCGGCTTGCCTGAGTTCGTCAGCGCCGACGCCGCGCTGGCTGGTGATCCAGGAACGACG
CGCGAGCACAACGAGATCAGCGTCAGCCAGAGCCTGATGATGGAACCCGCGCGACCTCCGCGACG
AGCGCGCCAACCTGTTCTGTCACACCGGGCAATGGCTGGAGTGGCTGGCGGCGACAGGGTGGCGACCT
GGCTTGTGGGGTGGTGCCGCGGGCAGCGCTCTCGACCTGCTTGGCTACGATGTCCTGCTGGCTCGC
TGCAAGACCGACCGCGCCCGCTGGAGCCGGCCGAGCTGCTGGCTTCGCTCGAAGCGCGGGTGGCGC
GCTACATGCTCCCGGCGCAGTTGCGCGTGTGCAACGCTGCGCGTCACCGGCAACGGCAAGATCGA
CCGCAAGGCCCTGACCGGCTTTCGCCCGCCAGCCCGAGCGGACCTTCGGCATGGCGTCCGCGAGGCA
CCGGCCGACGAACCTGGAGAATGCGCTGCTGGCACTCTGGCGGGAGGTGCTGGACAACCCGTCGCTGG
GCGTCGAGCAAGACTTCTTCGGGGCGCGCGGCGACTCGCTGTTGATCGCCAGTTGATCGCCCGTTT
GCGGCAACGACTGGAAGCGCCCGCTCGGCATCCGTTTCGATCGCTGCTACGCTGGGCGCTCAGCCAG
CCGACGCGCGCGCGGCTGGCCGAACGCTGCGCAGCGCGCGGGAAGAGGGCGCTGGGCGAGCCCTGG
CCGCGGCGCGCGGCTGCGCCCGGCGCGCGGCGCATGTCGCGCGCACCGCTCGCCGAGGGCGCGGT
GGCGCTCGACCCGCTGGTGCGCTGGTGCGCGGCGAGGGCGTGCCGCGGGTGCTGGTCCACGAAGGC
CTCGGCACGCTACTGCCGTACCGCCCGCTGCTTCGCGCCCTGGGTGAGGGGCGGCGCTTGTGGGGC
TGGCCGTGCATGACAGCGACGCTACCTGGCGATCCCGCGGAGCATCTCAACGCTGCTTCGGCCG
CCGCTACGCGGAGGCGCTCCATCGCGCGGGCTACGCGAGGTGACCTGCTCGGCTACTGCTCCGGC
GGGTGGTTCGCTGGAGACCGCAAGTCCCTGGTCCAGCGCGGGTGCGCGTGCGCCAACTGGATA
TCGCTTCCAGCTACCGGATTCCTTACCGGGTGGACGACGAGCGCTGCTGTTGTTTTCAGCTTCGCGC
GACCTTCGGCTGGATACCGCGGCGCTCGGCTTCCCCGCGCGGAAACGCTCTCGGCCAGGCGGTGCGAG
GCGGCGCTCGCGCAGACACCGGAGCGCTGGTTCGCGGAGGCGCTGGCGGGGTGCGGGGCTGGCCG
ATCTCGTTCGCTGCGCGGCGCTGCTACAGCGGCGAGCGGTAGCGCCGAGCGGCTCAGCGTTCGA
ACGCGACACCTCTACCGGCTGTTCTGTCGCGGACGCGGCAACCCATGGTGCGCGCTACGCGGAGG
CTCTGGAGACCAATGGCGGGCGCGCGCTTGGCGCGTGCGGCATCCACGAGGTGCGCGGGCGGCA
CTTCGACTGCTGGGCGAAGCCCTGGCGCAATCTTGTGCAACCCATGCCAGAGGAGGCGAGCCGA
TGA

```

The VIR16 protein (SEQ ID NO:32) encoded by SEQ ID NO:31 is presented using the one-letter amino acid code in Table 18B.

Table 18B. Encoded VIR16 protein sequence (SEQ ID NO:32)

```

MSLGELLETCRSRIELWSEAGRLRYRAPQALDAGLAERLRAEREALLEHLEGGPGWRAEPM
HQRFPPLTPVQAAYVLGRQAADFYGGNACQLYAEYDWPADTDPARLEAAWNAMVERHPMLRAVIED
NAWQVRVLPVWPQRLTVHACAGLDEAAAFQAHLERVRLRDLHACAALDQWPVLRPELSIGRDACVL
HCSVDFTLVLDYASLQLLLGEWRRRYLDLPQWTAEPLATFRDYVGVEQRRRQSPAQRDRDWWLAR
LDALPGRPDLPLRVQPDTRSTRFRHFHARLDEAAWQALGARAGEHGLSAAGVALAAFAETIGRWS
QAPAFCLNLTVLNRPPLHPQLAQVLGDFLTALSLAVDSRHGDSFVERARRIGEOMFDDLDHPTFS
GVDLLRELARRRGRGADLMPVFTSGIGSVQRLLDGDEAPRAPRYMISQTPQVWLDCQVTDQFGG

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LEIGWDVRLGLFPEGQAEAMFDDFVGLLRRLAQSPRAWTDGDATEPVEAPPQALPGSARSIAAGF
AERALLTPDATAIHDAAGSYRQVAQHASALRRVLEAHGAGRGRVAVMLPKSAAQLVAVIGIL
QAGAAYVPVDIRQPPLRRQAILASAEVVALVCLESDVPDVGACVAIDRLAADSAPPPAAEVA
ADDLAYVIYTSGSTGTGPKGVMLSHAASNTLLDINQRYGVDANDRVLGLAELSFDLVDYDFFGAT
AAGAQQVLPDPARGSDPSHWAELLERHAITLWNSVPAQQQMLIDYLESEFQRHLPGRCVLWSGD
WIPVSLPTRWRRWPDLSALFSLGGATEAAIWSIEQPIRQHTELASIPYGRALRGQSVEVLDARG
RRCPPGVRGEIHIGGVGLALGYAGDPQRTAERFVRHPDGRRLYRTGDLGRYLADGSIEFLGREDD
QVKIRGHRIELAELDAALCAHPQVNLAATVVLGETHERSLASFVTLHAPVEAGEDPRTALDAVRQ
RAAQALRRDWGSEEGIAAVALDRACLASLAWLASGLFASATPLDLATLCQRLGIAEARQRL
LRHWLRQLEEGGYLRAEGEGWLGAERPAQSPEDAWTAFAGCAPAALWPAELVAYLRDSAQSLGE
QLAGRISPAALMFPQGSARIAEAMYSQGLHAQALHEAMAEATAAIVERQPQRRWRLLLELGAGTAA
ASRTVIARLAPLVQRGAEDVYLFDTVSSYFLAAARERFADQPWVRFGRFDMNGDLLDQGVAPHSV
DILLSSGALNNALDTPALLAGLRELLSADAWLVIQELTREHNEISVSQSLMMENPRDLRDERRQL
FVHTGQWLEWLAAQGGDLACGVVPPGSALDLLGYDVLARCKTDRARLEPAELLAFAVEARVPRYM
LPAQLRVLERLPVTGNGKIDRKALTGFAHQPADLRHGVAQAPADELENALLALWREVLNPNLSLG
VEQDFFGAGGDSLLIAQLIARLRERLESARRHPFDRLLRWALSQPTPRGLAERLRSAPEEGRGPA
LAAARGVAPAPAGMSRAPLAEGAVALDPLVRLVPGEGVPRVLVHEGLGTLPLPYRPLLRALGEGRP
LLGLAVHDSDAYLAI PAEHLNACLGRRYAEALHRAGLREVDDLGYCSGGLVALETAKSLVQRGVR
VRQLDIVSSYRIPYRVDDERLLLFSAATLGLDTAALGFPAPERLQAVQAALAQTPERLVAEAL
AGLPGLADLVALRGRVLQAASGSADAVSVERDTLYRLFCHSVRASQAEAPEPYVGALRLFPVDPAG
NPLVPRYAEALQWRRAALGACGIEHPGGHFDCLGEALAQSLSKPMPEEASR

```

MUT17

A *Pseudomonas* bacterial mutant (MUT17) was made by transposon insertion in a *P. aeruginosa* wild-type strain PT894. In the *Dictyostelium* growth assay, the mutated

5 microorganism was less virulent compared to an isogenic bacterial strain. The nucleotide sequence immediately following the transposon insertion was cloned and identified as the gene encoding putative ATP-binding component of the ABC transporter, pchH (PA4223). This gene encodes the VIR17 nucleic acid (SEQ ID NO:33) shown in Table 19A.

Table 19A. VIR17 Nucleotide Sequence (SEQ ID NO:33)

```

GTGACCCCGGTGCTGTGGCGCCTGCTGCGCACCTATCGCTGGCGGCTGGCGGCGGCCATGGGGTTGC
AGGCCCTGGCCGGGCTCTGCTCGCTGTGTCCTGGATGCTTCTCGCCTGGCTCGCCGAGCCGCTGGC
GCGCGCCAGGCGCAGCCGGCCCTGCTGGCCCTGGTGTGCTGCTGGCGGTGCTGGCGGCTGGCTGGC
CAGGCGCTGGCCGCGCACCTGGCCACCGGGTCGACGCGGACCTCTGCAACGACCTGCGCCTGCGCC
TGCTGGCGCACCTGCAACGGCTGCCGCTGGACTGGTTCGGTTCGCCAGGGCCCGGACGGCGTGGCGCG
CCTCGTGGAGCAGGACGTGCGGGCCCTGCACCACTGATCGCGCACGCTCCCAACGATCTCAGCAAC
CTGTTGGTGGTGGCGCTCGCTCGCGTTGCTCTGGCTGGCTGGCTGCAACCTGGCTGCTGCTGTTCT
GCCTGCTGCCGCTGGTGTGCTGGCGCGCGCGGCTTCCTGCTGCTGCGCTCGCGCGGCTACCGCGACCT
GGTGTGCGCGCGCAACGCGCGCTGGAAAGGCTCTCGGCGGACTATGGCGAATTCGCCACCAACCTG
CTGCTGGCCCGACAGTACCCCGGCGCGCGCATACAACAGGGCGCGGAGGCGTGGCGGGCGGCTTCG
GCGAAGCGTTCCGGCGCTGGGTGAAGCGGGTCGGCCACCTCGCCGCGCTGGTCTACGTGCAGTTGTC
GACGCCCTGGCTGTGCTGGCTGGCTGGCTGGCTGGCTGGCTGGCTGGCTGGCTGGCTGGCTGGCTGG
GCGCTCGGCCAGGCTGTGCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG
GCCACGCGCGCGACGCGCTGCTGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG
GGCGCGCTGGCGCGAGGGCCGCTCGACCCGCGAGCCGGTTCGATGGCGCGGTGGCGCTGCACGGCTG
GGCATGCTATGAAGGCGTGGAGGTCTGGCCGATATCGATCTGGAGCTGGAGGATGGCAGCCTGG
TGGCCCTGGTGGTCCCTCGGGCTCCGGCAAGACACCTGCTGCACCTGCTGGCGCGCTACATGGA
CGCGCAGCGCGGCAACTGGAGGTGGCGGCTGGCACTGAAGGACATGCTGATGCTGCTGCTGCTGCTG
CGGCATATCGCGCTGGTTCGGCCAGCAGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG
TGTTCCGCCCCGATGCCGATCTCCAGGAGATTGCCAGGCGCGCGCGCGCGCGCGCGCGCGCGCGCG
CATCATGGCCCTGGCGCGTGGCTACGACAGCGTGCCGGGACGCGACCTGCAACTGTCCGGCGCGCGAA
CTGCAACGACTGGCCCTGGCCCGTGGCTGCTATCGCCGCGGAGCCTGTTGCTGCTGCTGCTGCTGCTG

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CCTCGGCGCTGGATCCGACACCGCCCGGCAGGTCTTGGCGAACCTGCGCGAACGCGGCGGTGGCCG
 GACCCGGGTGATCGTCGCCCATCGTCTGGCCGAAGTCAGCGATGCCGACCTGATCCTGGTGGTGGTC
 GCTGGCCGTCTGGTGAACGCGGCGAGCAGCGGCGCTGTGGCGGCGGACGGCGCCTATGCGCGCT
 TGTGGCGTGAACAGAACGGCGCGGAGGTGGCGGCATGA

The VIR17 protein (SEQ ID NO:34) encoded by SEQ ID NO:33 is presented using the one-letter amino acid code in Table 19B.

Table 19B. Encoded VIR10 protein sequence (SEQ ID NO:34)

MTPVLWRLRLRTRYRWRLAAAMGLQALAGLCSLLPWMLLAWLAEPLARGQAQPALLALVLLAVLAWL
GCQALAAHLAHRVDADLCNDLRLRLLAHLQRLPLDWFGRQPGDVGARLVEQDVRLHQLIAHAPN
DLSNLLVVPLVALLWLAWLHPWLLLLFCLLPVLAAAGFLLRLSARYRDLVLRRNAALERLSADYG
EFAHNLLLARQYPGAGIQQGAEEASAAAFGEAFGAWVKRVGHLAALVYVQLSTPWLLAWVLLGALA
LDALGVPLALGQACAFLLLLRALAAPVQALGHGGDALLGARAAERLQQVFDQAPLAEGRSTREP
VDGAVPLHGLGHAYEGVEVLADIDLEEDGSLVALVGPSSGSKSTILLHLLARYMDAQERGELEVG
LALKDMPDAPVRRHRHIALVQQAALAEISLADNLAI FRPDALDQEI RQAARDACLDERIMALPRGY
DSVPGRDLQLSGGELQRLALARALLSPASLMLLDEPTSLDPQTARQARLRLNRERGGGRTRVIVA
HRLAEVSDADLILVLVAGRLVERGEHAALLAADGAYARLWREONGAEVAA

The role of VIR17 in virulence was confirmed using phage to retransduce this mutation into the wild-type PT894 strain where attenuated virulence was again observed in the *Dictyostelium* growth assay compared to an isogenic bacterial strain.

MUT18

A *Pseudomonas* bacterial mutant (MUT18) was made by transposon insertion in a *P. aeruginosa* wild-type strain PT894. In the *Dictyostelium* growth assay, the mutated microorganism was less virulent compared to an isogenic bacterial strain. The nucleotide sequence immediately following the transposon insertion was cloned and identified as the gene encoding the putative ATP-binding component of ABC transporter, pchI (PA4222).

This gene encodes the VIR18 nucleic acid (SEQ ID NO:35) shown in Table 20A.

Table 20A. VIR18 Nucleotide Sequence (SEQ ID NO:35)

ATGACCCCTGTTTCGAACGAATGCGTGCGCTGCCCGAAGACTGCCGTGCCGCGTTGCGCCGGGCGAGCG
CC'TGGGCGGGTCC'TGGCGGGCGCTGCTGGACGCCGCTTGCGGGCGTATTGCTGGTGCCGTTGGTTCGAGGC
CTGGTTTCGCCGAAGCGCGCTTGCCCTGGCGCTGGGTTCGCCGCGCTTGCTCGGCTTGAGCCTGGCGCAG
GCGCTGTTGCACTACCTGGCCCTGCGCTGCGGTTTCGCGCCGGCGGGCTCGCTGGCGCTGGAGCTGG
TGC GCAGCCTGGTGGCGCGCTTGCCGCGCGCTGGCGCCGCGCGCTGCGCGGCTGCGCGCGCCGA
AGGCCGTGCTGCGCGCGCCGGTGATCGAGGCGATGGGCATTCCGGCGCACCTGCTGGGGCCGCTGATC
CGCGCTTGGTGACGCCGCTCGGGTGATCTCGGGCTGTTCCTGATCGACCCGCTCCATCGCCCTCG
GCCTGCTCC'TTGTGGTGCC'TTCTCGCGCGCTGTTGCGCTGGAGCGGGCGCGCAATCTGGCGCG
GGAGGATGCCCGGCTGGCCGCCGAGCGCGACGCCGACGGCAGTTCGAGGCGTTTCGCCGAACGCCAG
CCACTGCTGCGCGCGCGCGAGCGCGAAAGCGCTGCCCGCCAGGGGCTGGAAGAGGCCTTGCGCAGTC
TCCACCGCAGCACCTTGGATCTGTTGCGGCGCAGCCTGCCACGCGGCTCGGCTTCGCCCTGGCGGT
GCAGGCGGCGTTTCGCCCTTCGCCCTGCTCGCGCGCGCTTGGCGGTGGAGCGGCAATGGCTGGACGGC
GCTCGGCTGGTGGCGCTGCTGGTGCTGCTGGTGCGCTTCATCTGAGCCGCTGGCCAGCTACCCATC

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TCGACCAGGCGTTGCGCGGCGCCTGGCAGGCGCTGGATACCTGCTGCGGGTTTTTCGCCCTGGCTCC
GCTGCGCAGCCCCGAGCCGGGCGAGCGGCGCACGACGCCAGCCTGGCGGGCCGAGGCGGTGGAATTG
CGCCTGGAAGATGGCCGCGCCTTGCTCGAGGACATTTCCCTGAGGCTGGAGCCGGGTTTCGCTGAACG
TCCTCGTCGGACCTCCGGGGCCGGCAAGAGCAGCCTGCTGGCGCTGCTCGGGCGGCTCTACGACGT
CGATGCCGGGCGTGTCTGCTGGGTGGCGTGGATATCCGCCGGTTGAGCGAAACGACCCTCGCCGCC
AGTCGTAACCTGGTGTTCAGGACAACGGCCTGTTCCGCGGCAGCGTTGCCTGGAACCTGCGCATGG
CGCGAGCGGACGCCGATCTCGAAGCGCTGCGCGAGGCGGCGCGGGCGGTTGGCCTGCTGGAAGAGAT
CGAGGCCTGGCCGCGAGGCTGGGACAGCGACGTGGTCCCGCGGCGCGCTGCTGCTCGACGAGCCCA
CGGCAACGCCTGTGCTGGCTCGCGGGCTGCTCTCGACGGCGCGGTTGCTGCTGCTCGACGAGCCCA
CCGCCAGCCTCGACGCCGCCAGCGAGGCGCAGGTGCTGCGCAGCCTGCTCGGGTTGCGCGGGCCGGCG
CACCTGCTGGTAGTGACCAACCGCCCGGCGCTGGCGCGTCAAGCCGACCAGGTACTGCTGCTGGAG
GAGGGGCGCCTGCGCCTCAGCGGACTTCACGCCGATCTGCTCGTCCGGGACGACTGGTATGCCGGTT
TCGTCGGGCTGGCGGGCGAGGAAAGTTCCGCGACGGTTCGTGGATCGATAG
```

The VIR18 protein (SEQ ID NO:36) encoded by SEQ ID NO:37 is presented using the one-letter amino acid code in Table 20B.

Table 20B. Encoded VIR18 protein sequence (SEQ ID NO:36)

```
MTLFFERMALPEDCRAALRRASAWAVLAALLDAACGVLLVPLVEAWFAEGALPWRWVAALLGLSL
AQALLQYLALRRGFAAGGSLAAGLVRSLVARLPRLAPPALRRVAPAEGLLRGPMQAMGIPAHL
GPLIAALVTPLGVILGLFLIDPSIALGLLLAGAFIAALLRWSGRRNLAAEDARLAAERDAARQLQ
AFAERQPLLRRAAQRESVARQGLEEALRSLHRSTLDLLRRSLPSGLGFALAVQAAFAFALLGGAWA
VERQWLDGARLVAVLVLLVRFIEPLAQLTHLDQALRGAWQALDTLRLVFALAPLRSPEPGERPHD
ASLAAEAVELRLEDGRALLEDISLRLEPGSLNVLVGSPGAGKSSLLALLGRLYDVDAGRVLGGV
DIRRLSETTLAASRNLFVQDNGLFRGSVAWNLRMARADADLEALREAAAVGLLEEIEAWPQGW
SDVPGGALLSGGQRQRLCLARGLLSTAPLLLLDEPTASLDAASEAQVLRSLGLRGRRTLLVVT
HRPALARQADQVLLLEEGRLRLSGLHADLLVRDDWYAGFVGLAGEESSATVVDR
```

The role of VIR18 in virulence was confirmed using phage to retransduce this mutation into the wild-type PT894 strain where attenuated virulence was again observed in the *Dictyostelium* growth assay compared to an isogenic bacterial strain.

MUT19

A *Pseudomonas* bacterial mutant (MUT19) was made by transposon insertion in a *P. aeruginosa* wild-type strain PT894. In the *Dictyostelium* growth assay, the mutated microorganism was less virulent compared to an isogenic bacterial strain. The nucleotide sequence immediately following the transposon insertion was cloned and identified as a gene cluster encoding the *P. aeruginosa* serotype O9 putative O-antigen biosynthesis pathway (VIR19). The insertion site nucleic acid sequence identifying the VIR19 gene in MUT19 is shown in Table 21.

Table 21. MUT19 Transposon Insertion Site (SEQ ID NO:37)

```
CTCTTTCAGCCGCACGCGGCGCACCTCGTGTGTGATCAGTGAGTGGTTTGCAACTGCGGGTCAAG
GATCTGGATTTCCTCACANGTNCGATCATCGTCGGGAGGGCAAGGGCTCCAAGGATCGGGCCCT
TGATGTTACCCGAGAGCTTGGCACCCAGCCTGCGCGAGCAGGGNNAATTGATCCGGTGGATGACC
```

```

TTTTGAATGACCTTTAATAGATTATATTACTAATTAATTGGGGACCCCTANAGGTCCCCTTTTTTA
TTTTAAAAATTTTTTCACAAAACGGTTTATTNCCATAAAGCTTGCTCAATCAATCACCNATATCCN
CGGGAATTCGGCCTAGGCGGCCAGATCTGATCAAGAGACAGACCTCCAGCTTTCATCCGGAGCG
ACCACACGAGCGAGGTCAGTCACCTTTCATCGAAGGAATTTCTTGACATAGATCTCACCACCTTC
CATGTCCTCAAAGGCATGCCACACTAACTCGACGCCCTCCTCCAAAGAAATCATGAACCGGGTCA
TCCGCTCATCAGTGATAGGCAAGACGCCCTTGTCCTTG

```

The role of this cluster in virulence was confirmed using phage to retransduce this mutation into the wild-type PT894 strain where attenuated virulence was again observed in the *Dictyostelium* growth assay compared to an isogenic bacterial strain.

5

B. Attenuated *Klebsiella* Mutants

MUT20

A *Klebsiella* bacterial mutant (MUT20) was made by transposon insertion in a *Klebsiella* sp. wild-type strain. In the *Dictyostelium* growth assay, the mutated microorganism was less virulent compared to an isogenic bacterial strain. The nucleotide sequence immediately following the transposon insertion was cloned and identified as the gene encoding a hypothetical transcriptional regulator in met G-dld intergenic region (VIR20). The insertion site nucleic acid sequence identifying the VIR20 gene in MUT20 is shown in Table 22.

15

Table 22. MUT20 Transposon Insertion Site (SEQ ID NO:38)

```

ACGCAGGATATCTTCTTCATCAAATTTGTCGATGCCCGCCTTCGCTACGCTGCGGTTTCAGTAGACCG
TAACGACGCTGCCAGGCGCGCAGTGTGACCGGATTGATTCGCAACGTTTCGGCGACTTCACCGATAC
TGTAACACGCCATAGCAGCCTCACATCAACCTGATACCTTAATACCTAACTAACGAATTCAGGCAT
CCTGTACAACCTCTATTTTCTTGTACAGATAAAGATATCAGGTTGCGGCTCACAGCGCCCGGAAAAA
AGATGAAAAAATGTTTAGCTGATTTTCGCGGTGTTTCATTTTCTTCCGGCCATGCGACGGCGGGTAG
GCCCCCAGGCGCGCGCTGGCGAACAAATTCGCTGAAACTGTGAAATACCGGCTGATTCAGCCAC
ATCCACTCTTCAGACGCTCAACGCCGACGGCTGAGACCGCAATCTCCAGAGAAGTACAGCATTTGA
TAATCGCCTG

```

MUT21

A *Klebsiella* bacterial mutant (MUT21) was made by transposon insertion in a *Klebsiella* sp. wild-type strain. In the *Dictyostelium* growth assay, the mutated microorganism was less virulent compared to an isogenic bacterial strain. The nucleotide sequence immediately following the transposon insertion was cloned and identified as the gene encoding •-cystathionase (VIR21). The insertion site nucleic acid sequence identifying the VIR21 gene in MUT21 is shown in Table 23.

20

Table 23. MUT21 Transposon Insertion Site (SEQ ID NO:39)

GACCATGTGCTGATGACCAATACCGCCTATGAGCCAAGCCAGGACTTTTGTACCAAAATTCGCGCA
 AACTCGGCGTCACCACCAGCTGGTTTCGATCCCTTAATCGGCGCCGATATCGCCCGTCTGGTTCGCCC
 TGAGACCCGCGTGGTGTTCCTCGAATCGCCCGGCTCGATCACCATGGAAGTGCACGATGTGCCGGCG
 ATAGTCGCCCGCGTGCCTCAGGTCGCCCCGGAAGCGATTATCATGATCGATAACACCTGGGCGGCGG
 GGATCCTGTTTAAAGCCCTGGATTTTGGCATTGATATTTCCATTACAGGCAGGCACCAAATACCTGAT
 CGGCCATTCCGACGCCATGGTGGGCACCGCGGTGGCGAACGCGCGCTGC'TGGCCGCGAGCTGCGTGAA
 AATGCC'TACCTGATGGGGCAAATGCTGGACGCCGATACTGCC'TATATGACCAGCCGCGGCTGCGAA
 CCCTGGGCGTGCCTGCGTCAGCATCATGAAAGCAGCCTGCGCATC

MUT22

A *Klebsiella* bacterial mutant (MUT22) was made by transposon insertion in a
 5 *Klebsiella* sp. wild-type strain. In the *Dictyostelium* growth assay, the mutated
 microorganism was less virulent compared to an isogenic bacterial strain. The nucleotide
 sequence immediately following the transposon insertion was cloned and identified as
 ribosome binding factor A (VIR22). The insertion site nucleic acid sequence identifying the
 VIR22 gene in MUT22 is shown in Table 24.

Table 24. MUT22 Transposon Insertion Site (SEQ ID NO:40)

CTTTTGGCCCTTTTTTGTCTTTATTC'TGGAGAACTTATTATGGCGAAAGAATTTGGTCGCCCCGAG
 CGTGTGGCCCAGGAGATGCAAAAAGAGATTGCCATCATCCTGCAGCGTGAAATTAAAGATCCGCGTC
 TGGGCATGATGACCACCGTTTCCGGTGTGGAAATGTCCCGTGACCTGGCCTATGCCAAGGTGTATGT
 CACCTTCCTTAACGACAAAGATGAAGCCGCGGTGAAAGCGGGCATCAAAGCGCTGCAGGAAGCTTCT
 GGCTTTATCCGCTCTCTGCTGGGGAAAGCGATGCGTCTGCGCATCGTACCGGAACTGACTTTCTTCT
 ACGACAAC'TCACTGGTGAAGGGATGCGTATGTCCAACCTGG

MUT23

A *Klebsiella* bacterial mutant (MUT23) was made by transposon insertion in a
 15 *Klebsiella* sp. wild-type strain. In the *Dictyostelium* growth assay, the mutated
 microorganism was less virulent compared to an isogenic bacterial strain. The nucleotide
 sequence immediately following the transposon insertion was cloned and identified as the
 gene encoding aspartokinase/homoserine dehydrogenase (VIR23). The insertion site nucleic
 acid sequence identifying the VIR23 gene in MUT23 is shown in Table 25.

Table 25. MUT23 Transposon Insertion Site (SEQ ID NO:41)

GCCCAGCCCGCTTTCCCGCTTGCCAGTTAAAGCCTTCGTGGAGCAGGAATTTGCTCAGATTAAGC
 ATGTTCTGCACGGCATCAGCCTGCTGGGTGAGTGCCCGGACAGCGTCAATGCCGCGCTGATCTGCCG
 CGGCGAAAAGCTCTCCATCGCCATCATGGCGGGTCTGCTGGAAGCCCGTGGACACAAAGTCAGTGTC
 ATTAACCCGGTCGAAAAACTGCTCGCCGTGGGTCACTATCTGGAATCCACCGTCGATATCGCCGAAT

```
CCACCCGCCGCGATTGCCGCCAGCCAGATCCCGGCAGACCATATGATCCTGATGGCCGGGTTTACCGC
CGGCAATGAGAAAGGCCGAGCTGGTGGTGCTGGGGCGTAACGGCTCCGACTACTCGGCTGCGGTACTG
GCCGCTGCTGCGCGCTGACTGCTGCGAAATCTGGACCGATGTCGACGGAGTGACACCTGCGATC
CGCGTCAGGTGCCGGATGCGCGCTGCTGAAATCGATGTCTTATCAGGAGGCGATGGAGCTCTCCTA
CTTTGGCGCGAAAGTGCTGCACCCGCGCACCATTGCCCTATCGCCAGTTCCAAATCCCATGCCTG
ATTAATAATACCGGCAACCCCC
```

MUT24

A *Klebsiella* bacterial mutant (MUT24) was made by transposon insertion in a *Klebsiella* sp. wild-type strain. In the *Dictyostelium* growth assay, the mutated microorganism was less virulent compared to an isogenic bacterial strain. The nucleotide sequence immediately following the transposon insertion was cloned and identified as the gene encoding cystathione • -synthetase (VIR24). The insertion site nucleic acid sequence identifying the VIR24 gene in MUT24 is shown in Table 26.

Table 26. MUT24 Transposon Insertion Site (SEQ ID NO:42)

```
GGCGCAGCGTCTGCTCGTCACCGTCAAGCTCGAAGCTTAACATTGCGCCAAAACCTTTTGTGACG
CGCCGCAATTTTCATGCCCCCTGGTTTTCCGGCAGCGATGGATGATACAGCTTTTTCACCAGCGGTGG
GTTTTTCAGATACTCAACGATCGCCAGGGCATTTCGCTGCGCCACTTCCATCCGTGGAGACAGCGTCC
GCAGCCCGCGCAACAGCAGATAGCTGTGCAAGGCGCTGCCGGTGACGCCAATATTTATTCGCCCACCA
TGCCAGTTCCGGTGACAGTTGCCGGATCTTTGGCAATCACCACCCCGGCCACCACATCGGAGTGACCA
TTGAGGTATTTGGTACAGGA
```

MUT25

A *Klebsiella* bacterial mutant (MUT25) was made by transposon insertion in a *Klebsiella* sp. wild-type strain. In the *Dictyostelium* growth assay, the mutated microorganism was less virulent compared to an isogenic bacterial strain. The nucleotide sequence immediately following the transposon insertion was cloned and identified as the gene encoding phosphoribosylformylglycinamide synthase (VIR25). The insertion site nucleic acid sequence identifying the VIR25 gene in MUT25 is shown in Table 27.

Table 27. MUT25 Transposon Insertion Site (SEQ ID NO:43)

```
GTTGCGTCCAGGCGGGTAAACGCATCCTGCAGGTAGTCAATTTGCTCGTCGGCCAGCGCCAGACCC
AGACGGAGGTTGGCGTCAATCAGCGCTGACGCCCTTCGCCCAGCAGGTCGACGCTGGTGACCGGCG
TCGGCTGATGGTGAGCGAACAGCTTCTCGCCCGCTTCCAGCTCGTCGAAGACGCTCTCCATCATGCG
GTCATGCAGCTCCGCCGCCACCGCGGCCACTGCGCTTCGGTCAGGGTTGAGGCTTCAACGTAATAC
GCCACGCCGCGCTCAAGACGCACAACCTGCGCCAGACCGCAGTTGTGAGCGATATCGGTAGCTTTAG
AAGACCAGGGAGAGATGGTGCCAGGGCGAGGGTCAAGAGCAGTAATTTACCGGTGCGGGTATGGCT
GCTTAAGCTCGGGCCATACTGAAGCAGTCGCGCCAGGCGCTCGCGATCGTCAGCGCTCAGCGGGGCG
TTCAGATCGGCAAAATGAATATATTCGGCAT
```

MUT26

A *Klebsiella* bacterial mutant (MUT26) was made by transposon insertion in a *Klebsiella* sp. wild-type strain. In the *Dictyostelium* growth assay, the mutated microorganism was less virulent compared to an isogenic bacterial strain. The nucleotide sequence immediately following the transposon insertion was cloned and identified as the gene encoding homoserine transsuccinylase (VIR26). The insertion site nucleic acid sequence identifying the VIR26 gene in MUT26 is shown in Table 28.

Table 28. MUT26 Transposon Insertion Site (SEQ ID NO:44)

```
GTATTGGCATCGTACTCCTGGGCTGGCCGGTGACAAAGGCGATGCGCTTATCTTTGCTGGCGAACAA
ATACGCATCGCCCTCTTCCGTCTCCGCGAGGATCTCGAGATCGGTATAGTCGCGAATAAGTCCGGCC
GGAAAATCAGCATAGCGTGAGTGCGGGGCCAGGAAAGAGTCGTCGAAACCGCGGGTCAGTAAGGCGT
GCGGATGAAGAATATGGTGTTCATAGACGCCGGAATCTTTTCGGCGCGGGTCTGCTTGGGAATGCC
GTACAGAATGTTAGCGCGGCCGTAACCGCCCAACAGACGAACAGCGTCGAAGTGACGTGATCCTTG
GCCCCACTCCAGCACCTGTTTGATCTGCGGCCAGTAAGCAACATCGTTAAACTCAACCAGGCCATAAG
GAGCGCCGGTAACAATCAGGCCGTCAAAGTTCGTATC
```

MUT27

A *Klebsiella* bacterial mutant (MUT27) was made by transposon insertion in a *Klebsiella* sp. wild-type strain. In the *Dictyostelium* growth assay, the mutated microorganism was less virulent compared to an isogenic bacterial strain. The nucleotide sequence immediately following the transposon insertion was cloned and identified as the gene encoding 3'-phosphoadenosine 5'-phosphosulfate reductase (VIR27). The insertion site nucleic acid sequence identifying the VIR27 gene in MUT27 is shown in Table 29.

Table 29. MUT27 Transposon Insertion Site (SEQ ID NO:45)

```
GAGGTTTCATATGTCCGTACTCGATCTAAACGCGCTTAATGCATTGCCGAAAGTGGAACGCATTCTGG
CACTCGCGGAAACCAACGCCCAACTGGAAAAGCTTGACGCCGAAGGGCGTGTGGCGTGGGCGCTGGA
AAATCTGCCGGGAAACTATGTGCTGTCGTGAGCTTTGGCATTCAGGCGGCGGTAAGTTTGCATCTG
GTGAATCAGATCCGCCCCGACATTCGGGTGATCCTCACCGATACCGGCTACCTGTTCCCGGAAACCT
ATCAGTTTATTGACGAGCTGACGACAAG
```

MUT28

A *Klebsiella* bacterial mutant (MUT28) was made by transposon insertion in a *Klebsiella* sp. wild-type strain. In the *Dictyostelium* growth assay, the mutated microorganism was less virulent compared to an isogenic bacterial strain. The nucleotide sequence immediately following the transposon insertion was cloned and identified as the

gene encoding Sfi protein (VIR28). The insertion site nucleic acid sequence identifying the VIR28 gene in MUT28 is shown in Table 30.

Table 30. MUT28 Transposon Insertion Site (SEQ ID NO:46)

```
TGTTAAAGCGTGCGTTCTACAGCCTGTTAGTCCTGCTCGGCCCTGCTGCTGTTGACCGTGCTGGGCCCT
TGACCGCTGGATGAGCTGGAAAACCGCGCCCTATATCTATGATGAACGTCAGGACCTGCCCTACCGT
CAGGTCGGTGTGGTGCTGGGCACCGCCAAATATTACCGCACCGGCGTCATCAATCAGTATTACCGTT
ACCGCATCCAGGGTGCGCTGAACGCCTACAACAGCGGCAAGGTCAACTATCTCCTGCTGAGCGGCGA
TAATGCTCTGCAAAGCTACAATGAACCGATGACCATGCGTCGGGACCTGATTAAAGGCGGCGTCGAT
CCCGCGGATATCGTACTGGACTATGCCGGTTTCCGTACCCCTCGACTCGATCGTCCGTACCCGGAAG
TGTTTCGACACCAACGACTTCATTATCATCACCCAGCGCTTCCACTGCGAACGGGCGCTGTTTATCGC
CCTGCATATGGGGATCCAGGCCCAAGTGCTACGC
```

5 MUT29

A *Klebsiella* bacterial mutant (MUT29) was made by transposon insertion in a *Klebsiella* sp. wild-type strain. In the *Dictyostelium* growth assay, the mutated microorganism was less virulent compared to an isogenic bacterial strain. The nucleotide sequence immediately following the transposon insertion was cloned and identified as the gene encoding transcriptional activator protein LysR (VIR29). The insertion site nucleic acid sequence identifying the VIR29 gene in MUT29 is shown in Table 31.

Table 31. MUT29 Transposon Insertion Site (SEQ ID NO:47)

```
CGCTGAACCTCCTCAAACAAACGCGAGGCCCTGCACCTGTCGGCTGCAGGCGACCAGCGTGATCCGC
TCAAACAGCTGCAGGCCGAGCACCTTCTCAAAGCGCGCCAGCTCGCGGCTGACCGTGGGTTGCGAGG
TGTGACGATCCGCGCCGCTTCGGTCAGGTTGCCGGTGGTCATCACCGCGTGAAAGATTTTCGATATG
ACGCAAATTGACGGCTGGCATGCGGCTCTCCGTGAGGCTCGGCTGGAACCATATCATTTTTGATAGA
GTCGCGATAAAACGATATTTTTTATTCGTCTGTCACTGTGGCGTAATCAGAAAAACAGCGACCAAC
ACACGCACTGCACCGGAGTTCTTATGCCACACTCGCTTTACGCCACCGATACTGACCTGACCGCGGA
CAACCTGCTGCGCCTGCCGGCGGAATTTGGCTGCCCGGTCTGGGTCTATGATGCGCAGATTATTCGC
CGCCAGATAGCCAGCTCAGCCAGTTTCGAC
```

MUT30

A *Klebsiella* bacterial mutant (MUT30) was made by transposon insertion in a *Klebsiella* sp. wild-type strain. In the *Dictyostelium* growth assay, the mutated microorganism was less virulent compared to an isogenic bacterial strain. The nucleotide sequence immediately following the transposon insertion was cloned and identified as the gene encoding TrpD (VIR30). The insertion site nucleic acid sequence identifying the VIR30 gene in MUT30 is shown in Table 32.

Table 32. MUT30 Transposon Insertion Site (SEQ ID NO:48)

GGCTTCCACCCAAATCGCTTTGTCGGCAACGATTTTTGCTAAAACGGCTTTGCATTCTTTACCCCTCT
 TGCCCGCTAAGTGCGGTCACTCTGTTCATAGGCCGCGCCGCTGCTGCAGCACATCCAGTACCTGCTGA
 GCGTTAGCTTTCAGATCTTCATGCCCGTGTAAACGCATCAATATGGCGACGTTGGCGGCGACGGCGG
 CTTGCTGAGCGGCTTCACCTTTACCTTG

MUT31

A *Klebsiella* bacterial mutant (MUT31) was made by transposon insertion in a
Klebsiella sp. wild-type strain. In the *Dictyostelium* growth assay, the mutated
 5 microorganism was less virulent compared to an isogenic bacterial strain. The nucleotide
 sequence immediately following the transposon insertion was cloned and identified as the
 gene encoding N-acetylglucosamine-6-phosphate deacetylase (VIR31). The insertion site
 nucleic acid sequence identifying the VIR31 gene in MUT31 is shown in Table 33.

Table 33. MUT31 Transposon Insertion Site (SEQ ID NO:49)

TGGCTCAACGCTGCTCAGTGGTGCGAGGTGTCACCTTTGGTGATCACATCGGCGTTGTCTGCACAGTG
 AAATCAGATCCAGCGCCGCGTCCGGTTTTACGCACGTAGTCCGGATTGTGGGTGCCTTTCTTAACGA
 TATTCAGCCACGGCCCTTCGAGATGCAGGCCAGCGCCTGGTTCGGATGTTTTTGCAGATATTCGCG
 CATCACGCGCACGCCCTTGCTTCATCAGATCGTCGCTGGAGGTAATCAGCGTCGGCAGGAAGCTGGTG
 CAGCCTGAGCGTTCGTTGGCCTTCTGCATGATCTCCAGCGTTTCGACAGTGACCGCCTCTGGGCTGT
 CGTTAAACTGCACGCCGCCGAGCCGTTGAGCTGGACGTCGATAAAACCGGGGGCGATTATTGCGCC
 GTTGACTGAGCGCTGCTCGATGTCAGACGGCAAATCTGCCAGCGGACAAAGACGTTTCGATAAAG

MUT32

A *Klebsiella* bacterial mutant (MUT32) was made by transposon insertion in a
Klebsiella sp. wild-type strain. In the *Dictyostelium* growth assay, the mutated
 15 microorganism was less virulent compared to an isogenic bacterial strain. The nucleotide
 sequence immediately following the transposon insertion was cloned and identified as the
 gene encoding WaaQ (VIR32; Regué *et al.* J. Bacteriol. 183(12): 3564-73, 2001). The
 insertion site nucleic acid sequence identifying the VIR32 gene in MUT32 is shown in Table
 34.

Table 34. MUT32 Transposon Insertion Site (SEQ ID NO:50)

TTAAGCACCATATCGTACCGCTGCTGGCGCAGCGTCTGAATGAGCTGCCATTGCATCTTCAGCTGAT
 ACCTTTTTCCCTGGCTTTTTCCAGCGGCGATCGAGACCATAAATATGGTGGATATCGGGGTTGGCTG
 CGAGCATATCCCGGCTCTCTTCATACAACAGGACATCCACGCTGGCGGCGGGGTACTGCTGTTTCAG
 CGCGTGAATAAGCGGCGTGATCAGCAGCATGTGCCATGATGGCGCAGCTTAATGACCAGGATCCGC
 GCCGGGTTCAACGGGCGCGGGAGAGGGTTTCAGGCGTCATACTCTGTCTTCATCCAGGATAAGGG
 TTCCGATTCTAGGGGATCAGACAGATTGAGAGAAGCGTTGTATTGCTCTACCATGACCCGATACGTA
 TGGCCTGAGGACGTTTTCTGTCACAATCCCGCAATTTCTCATCAGAT

MUT33

A *Klebsiella* bacterial mutant (MUT33) was made by transposon insertion in a *Klebsiella* sp. wild-type strain. In the *Dictyostelium* growth assay, the mutated microorganism was less virulent compared to an isogenic bacterial strain. The nucleotide sequence immediately following the transposon insertion was cloned and identified as the gene encoding 2-isopropylmalate synthase (VIR33). The insertion site nucleic acid sequence identifying the VIR33 gene in MUT33 is shown in Table 35.

Table 35. MUT33 Transposon Insertion Site (SEQ ID NO:51)

```
CACTCAGGCTTGCCTGTAACGCTTGTTCGCCATCACGTAAGGTCGTATCGAAAATAATGACTTGCTG
GCTCATGGTTTGGATCCTTAGTCTGTGTCTGGCGCCTTGTGACGAGCATAAAAAACCCGCGCCA
AGGCGCGGGTTTATAGTCTTGTCTGGAAGATGACTTAACGCTGAACGTCGCCCAACAGCCTACCGAG
CAAATGGCATGCGTTTAGTAGTAGTAGGCTGGTGATACGAGCGGTGCGAATCATTGCGTCAAACCTCC
AGATGAAATCGTTATGCTTTTAGAGTTACTGGATAGCCGTTTTAAAGTCAACCCCTGGCATGGAAAA
AGCGTTTTGGGCTGACTAAATGAATTAGCAAAATGTGCTGATGTAAGCCCCATTTGCCGAAGATCC
TATTTTGGACCGAAGGCGGTTTATCCCAATTTGTTTCATTTGAAAAA
```

MUT34

A *Klebsiella* bacterial mutant (MUT34) was made by transposon insertion in a *Klebsiella* sp. wild-type strain. In the *Dictyostelium* growth assay, the mutated microorganism was less virulent compared to an isogenic bacterial strain. The nucleotide sequence immediately following the transposon insertion was cloned and identified as the gene encoding histidinol dehydrogenase (VIR34). The insertion site nucleic acid sequence identifying the VIR34 gene in MUT34 is shown in Table 36.

Table 36. MUT34 Transposon Insertion Site (SEQ ID NO:52)

```
CGCTGAACCGCTATCCGGAGCCGCGAGCCGAAGTGCCGTGATTGAGAGCTACGCCCGCTACGCCGAGG
TCAAACCGGAGCAGGTGCTGGTCAGCCGCGGCGCCGACGAAGGCATCGAGCTGCTGATCCGCGCCTT
CTGTGAGCCCGGCGAAGACGCGGTGCTCTACTGCCCGCCGACCTACGGCATGTACAGCGTCAGCGCC
GAGACCATCGGCGTCGAGTGCCGCGACCGTGCCGACGCTGGCCAGCTGGCAGCTCGACCTGCCGGGCA
TCGAAGCGCGGCTGGACGGCGTGAAGGTGGTGTGTTGTCTGCAGCCCGAACAACCCGACCGGGCAGAT
TATCGACCCGCGATCGATGCGCGACCTGCTGGAGATGACCCGCGGCAAAGCCATCGTGGTGGCCGAC
GAAGCCTATATTGAATTCGCCCCGAGGCGACGCTCGCCGGCTGGCTCAGCGACTATCCGCACCTGG
TGGTGCTGCGCACGCTGTCCAAAGCCTTCGCCCTCGCCGGCCTGCGCTGCGGCTTCACCCTCGCCAA
CGCCGAGGTGATTAACGTGCTGCTGAAAGTGATCGCCCC
```

MUT35

A *Klebsiella* bacterial mutant (MUT35) was made by transposon insertion in a *Klebsiella* sp. wild-type strain. In the *Dictyostelium* growth assay, the mutated microorganism was less virulent compared to an isogenic bacterial strain. The nucleotide sequence immediately following the transposon insertion was cloned and identified as the gene encoding UDP-galactopyranose mutase (VIR35; Clarke *et al.*, J. Bacteriol., 177: 5411-18, 1995). The insertion site nucleic acid sequence identifying the VIR35 gene in MUT35 is shown in Table 37.

Table 37. MUT35 Transposon Insertion Site (SEQ ID NO:53)

```
CGTATATTTTCATCGTACAGAAACCGTAAACACAGGCATTGGCTGATTTTCAGTGAGTGAATTTAAAT
AGACTTCTGCCGTTTTCAATGCTTCGGCGATGGTCACATCCATATCAAGGTAACGGTAGGTTCCAAG
ACGACCGACAAAAGTGATGTTGGTTTCATTCTCGGCCAATGACAAATATTTTTCAAGAAGAGCCATT
TCTCCCATCTGGCGAATAGGATAGTAAGGAATATCATTTTCTTCACAAGCACGGCTATACTCTTTAT
AACAACAGAGCCGTCGTGTTGTTCCAGGGAGAAAAATATTTATGTTTCAGTGATGCGAGTATAGGG
CACATCCACAGAACAGTAGTTCATCACTGCGCATCCCTGG
```

MUT36

A *Klebsiella* bacterial mutant (MUT36) was made by transposon insertion in a *Klebsiella* sp. wild-type strain. In the *Dictyostelium* growth assay, the mutated microorganism was less virulent compared to an isogenic bacterial strain. The nucleotide sequence immediately following the transposon insertion was cloned and identified as the gene encoding O-antigen export system permease protein rfba (VIR36; Bronner *et al.*, Mol. Microbiol., 14: 505-19, 1994). The insertion site nucleic acid sequence identifying the VIR36 gene in MUT36 is shown in Table 38.

Table 38. MUT36 Transposon Insertion Site (SEQ ID NO:54)

```
GTACGCCGATTTTATATGCGTCTGATATGATTCCGGAAAAATTTAGCTGGATAATTACCTACAATCC
GCTAGCGAGTATGATTCCTTAGTTGGCGTGATTTATTCATGAATGGGACTCTTAATTTTGAGTATATT
TCTATACCTATTTTACGGGAATTATTTGACGGTTGTCGGTTTGTCTATTTTCAATAAAATTTAAAT
ATCGATTTGCAGAGATCTAAAAGTGCCTATAAGAGCAGCATGCTAGGCTATTTATGGTCAGTAGCA
AATCCATTGCTTTTTGCCATGATTTACTATTTTATATTTAAGCTGGTAATGAGAGTACAAATTCCTAA
ATTATACAGTTTTCTCATACCGGCTTGTTTCCGTGGCAATGGTTTGCCAGTTTCGGCCACTAAC
```

MUT37

A *Klebsiella* bacterial mutant (MUT37) was made by transposon insertion in a *Klebsiella* sp. wild-type strain. In the *Dictyostelium* growth assay, the mutated

microorganism was less virulent compared to an isogenic bacterial strain. The nucleotide sequence immediately following the transposon insertion was cloned and identified as the gene encoding uridyltransferase (VIR37). The insertion site nucleic acid sequence identifying the VIR37 gene in MUT37 is shown in Table 39.

5

Table 39. MUT37 Transposon Insertion Site (SEQ ID NO:55)

```
CGAGCCACCCACTGTAGCGTATGGATATCGCGCAAGCCGCCGGGGCTGCTTTTCACGTCCGGCTCGA
GGTTATAGCTGGTGCCATGATAGCGCTGATGACGGACGTTCTGCTCTTCGACCTTGGCGGCGAAGAA
CTTTTCCGATGGCCAGAAGCCGTCGCTAAAAATATGTTTTTGCAGTTCAAGGAACAGCGCGACGTCG
CCGATCAGCAGGCGCGATTTCGATTAAGTTGGTGGCAACGGTCAGATCCGAGAGACCTTCCAGCAGGC
ACTCTTCGAGGGTGCGTACGCTGTGGCCACCTCCAGCTTGACGTCCACAGCAGGGTGAGCAGTTC
GCCGACTTTTTTGCGCCCTGGTCCGCGCAGTTTTTTTACGACTGAGGATCAGCAGATCGACGTCTGAG
AGCGGGTGCGAG
```

MUT38

A *Klebsiella* bacterial mutant (MUT38) was made by transposon insertion in a *Klebsiella* sp. wild-type strain. In the *Dictyostelium* growth assay, the mutated microorganism was less virulent compared to an isogenic bacterial strain. The nucleotide sequence immediately following the transposon insertion was cloned and identified as the gene encoding pyridoxine phosphate biosynthetic protein PdxJ-PdxA (VIR38). The insertion site nucleic acid sequence identifying the VIR38 gene in MUT38 is shown in Table 40.

10

Table 40. MUT38 Transposon Insertion Site (SEQ ID NO:56)

```
CTTAACCCGACGCTGGCGAAGGCGGCCATATGGGAACAGAAGAGATAGACACCATCATTCGGGTGC
TGGAAGAGATGCGCGCAAAGGGGATGAACCTCAGCGGTCCGCTGCCGGCAGACACTCTCTTTCAGCC
GAAATATCTTGATCATGCCGATGCGGTACTCGCGATGTACCACGATCAGGGCCTGCCCGTGCTAAAA
TACCAGGGCTTTGGCCGCGGCGTGAACATTACGCTCGGTTTACCTTTTATTCGTACCTCCGTGCGACC
ACGGCACCGCACTGGAATTAGCGGGCCAGGGAAGCGGACGTCGGCAGTTTTATCAGCGGCGCTTAA
TCTCGCCATCAAAATGATTGTTAATACCCAATGAATAATCGAGTCCATCAGGGCCATTTAGCCCGCA
AACGCTTCGGGCAGAACTTCCTCAACGATCAGTTTGTGATCGACAGCATCGTCTCGGCGATTAAACC
GCAGAAAGGCCAGGCGATGGTTGAAATCGGC
```

15

MUT39

A *Klebsiella* bacterial mutant (MUT39) was made by transposon insertion in a *Klebsiella* sp. wild-type strain. In the *Dictyostelium* growth assay, the mutated microorganism was less virulent compared to an isogenic bacterial strain. The nucleotide sequence immediately following the transposon insertion was cloned and identified as the gene encoding triose phosphate isomerase (VIR39). The insertion site nucleic acid sequence identifying the VIR39 gene in MUT39 is shown in Table 41.

20

Table 41. MUT39 Transposon Insertion Site (SEQ ID NO:57)

```
GGGTCTGACCCCGGTTCTGTGCATCGGTGAAACCGAAGCCGAAAACGAAGCGGGCAAAACGGAAGAA
GTTTGCGCACGTCAGATCGACGCCGTGCTGAAAACCCAGGGCGCTGCCGCTTTTCGAAGGCGTGGTTA
TCGCTTACGAACCAGTATGGGCTATCGGTACCGGCAAATCAGCGACCCCGGCTCAGGCGCAGGCGGT
GCACAAATTCATCCGTGACCACATTGCTAAAGCTGACGCCAAAATCGCTGAGCAAGTGATCATCCAG
TACGGCGGTTCCGTTAACGCTGGCAACGCCGAGAGCTGTTACCCAGCCGGACATCGACGGCGCGC
TGTTTGGCGGCGCCTCCCTGAAAGCTGACGCTTTCGCGGTGATCGTTAAAGCAGCAGAAGCAGCGAA
AAAAGCGTAATTCGCTTTTCCCGGTGGCGACACGCGACCGGGTTGACTGACAAAACGTGGGAGCCCG
GCCT
```

MUT40

A *Klebsiella* bacterial mutant (MUT40) was made by transposon insertion in a *Klebsiella* sp. wild-type strain. In the *Dictyostelium* growth assay, the mutated microorganism was less virulent compared to an isogenic bacterial strain. The nucleotide sequence immediately following the transposon insertion was cloned and identified as the gene encoding aldehyde dehydrogenase (VIR40). The insertion site nucleic acid sequence identifying the VIR40 gene in MUT40 is shown in Table 42.

Table 42. MUT40 Transposon Insertion Site (SEQ ID NO:58)

```
GGTGGCGCACCTGGCGTCGTTTGTGTAGAAATTATGAATATTAATACCAGGAAAATTCCTAATTTT
TGTGTACGCTCTGACGAGCGCACAAATAAACAAGACGAATTTTGAACAATTGTCTTTAAATTTGTT
AATTGAATTGATCTGTTGTTGTTTAAAGGTATTTGAATTTCTTTTGTATAGATATGTAAATTAACAT
TGAAAAGCCATTTCAAAAATTAAATATATGGCGAACATAGCTATTAACCTATAGTTAACATCTTCCC
GGGTTGCCTTTTGATACTTCGGGTAATATATTTATTTTCGCACATCAAAATAACTCTTTTCTTCTG
TTTGTATTTCATGGCCATCTATTGGCGAAATAAGGCAGAGTAGAGGGGGATGTGCCTAATATCCTGC
GGAAGGAACGCAATGTACATTTACAGGGAGGAGCTGACGAGCCGTTTCGCGATAGCTTTAG
```

MUT41

A *Klebsiella* bacterial mutant (MUT41) was made by transposon insertion in a *Klebsiella* sp. wild-type strain. In the *Dictyostelium* growth assay, the mutated microorganism was less virulent compared to an isogenic bacterial strain. The nucleotide sequence immediately following the transposon insertion was cloned and identified as the gene encoding galactosyl transferase (VIR41; Clarke *et al.*, J. Bacteriol., 177 : 5411-18, 1995). The insertion site nucleic acid sequence identifying the VIR41 gene in MUT41 is shown in Table 43.

Table 43. MUT41 Transposon Insertion Site (SEQ ID NO:59)

```
TTGGTGGTGTGCTCGCGAAGAAATTTAATCTGCCGGTCATCGTAAGTTTGTGGGCTTGGAAGAGT
```

```

ATTTTCTTCTGACAGCATGCCTTTAAAATTATTGCGGCAGTTTACTATTGCTGCATATAAATATATT
GCCAGTAATAAGCGCTGTATATTTATGTTTGAACATGACCGCGACAGAAAAAACTGGCTAAGTTGG
TTGGACTCGAAGAACAACAGACTATTGTTATTGATGGTGCAGGCATTAATCCAGAGATATACAAATA
TTCTCTTGAACAGGATCACGATGTCCCTGTTGTATTGTTTGCCAGCCGTATGTTGTGGAGTAAAGGA
CTGGGCGACTTAATTGAAGCGAAGAAAATATTACGCAGTAAGAATATTTCACTTTACTTTGAATGTTG
CTGGAATTCTGGTCGAAAATGATAAAGATGCAATTTCCCTTCAGGGTCATTGAAAATTGGCATCAGC
AAGGATTAATTAAGTGGTTAGGTCGTTTCAATAATGTTTGCGATCTTATTGAGCAAT

```

MUT42

A *Klebsiella* bacterial mutant (MUT42) was made by transposon insertion in a *Klebsiella* sp. wild-type strain. In the *Dictyostelium* growth assay, the mutated microorganism was less virulent compared to an isogenic bacterial strain. The nucleotide sequence immediately following the transposon insertion was cloned and identified as the gene encoding siroheme synthetase (VIR42; Kolko *et al.*, J. Bacteriol., 183 : 328-35, 2001). The insertion site nucleic acid sequence identifying the VIR42 gene in MUT42 is shown in Table 44.

Table 44. MUT42 Transposon Insertion Site (SEQ ID NO:60)

```

TTACTTGCCCCCTTTTGGCCGAAC TGAACAAAGGCCCGTGC TGGTGATCGGCGGCGGCGAGATTGCT
GAACGTAAGATCAAGTTCC TGC TGC GCGCC CAGGCGCAGGTGCAGGTGGTCGCTGAAACGCTGTCAC
CGGCGCTGGCCGATCTGGCTGCGCGCCAGGCAC TCAGCTGGCGGGCGACGGCATT CAGCGACTCGCT
GGTGGATGATGTC TTTCTGGTGATTGCGGCCACCGAGGATGAGGCGCTTAACCAGCGGGTGTGTCG
GCAGCTAACGCGCGCTACCGGTTGGTCAACGTGGTGGATAACCAGGCGCTGTGCTCGTTTGTGTTCC
CTTCTATCGTCGACCGTTGCGCGCTGCTGGTGGCGATCTCCTCCAGCGGTAAAGCGCCGGTGTGTC
GCGCATTTCTGCGTGAAAAATCGAAGCGCTGCTGCCGACGAATCTCGGTGCGCTGGCGGAATCAGCA
AGCT

```

MUT43

A *Klebsiella* bacterial mutant (MUT43) was made by transposon insertion in a *Klebsiella* sp. wild-type strain. In the *Dictyostelium* growth assay, the mutated microorganism was less virulent compared to an isogenic bacterial strain. The nucleotide sequence immediately following the transposon insertion was cloned and identified as the gene encoding 7,8-dihydro-6-hydroxymethylpterin-pyrophosphokinase (VIR43). The insertion site nucleic acid sequence identifying the VIR43 gene in MUT43 is shown in Table 45.

Table 45. MUT43 Transposon Insertion Site (SEQ ID NO:61)

```

AGCAGGGCAATGGTGGTCGGTTTCATAACATTTCTTGATGATGAAAGTCATATTAACCGGCATTCTA
ACAGCAGCATTCAGAGGGGCAATGATTTTGGGCAACCGATTACGACGATCGCCGCAAATGCTAAAAA
AGGGAGAGGGGATTACAGCTGGCGGGCTTTTCCGCGCCGAGATTATCCAGCACGGCGCGCAGCGCC
AGGCCGTCAGGAAAGTGAAGGTCCGGGGCGATCTCGAACAGCGGCCAGAGCATAAAGCCGCGGTTTT

```

TCATATCGTAGTGCGGAACGGTCAGGCGCTCGCTGTTAATGACAGCATCGCCAAACAGCATGATATC
 GAGGTCCAGCGTGCGCGGCCCCAGCGTTTCGGCTTTGCGCACTCGCCCTGCTGCAGTTTCGATGCGC
 TGAGTATGATCGAGCAGCGTCTCGGGGGCAGGCGGTTTCCAGCGCAA

MUT44

A *Klebsiella* bacterial mutant (MUT44) was made by transposon insertion in a *Klebsiella* sp. wild-type strain. In the *Dictyostelium* growth assay, the mutated
 5 microorganism was less virulent compared to an isogenic bacterial strain. The nucleotide sequence immediately following the transposon insertion was cloned and identified as the gene encoding glucose-6-phosphate isomerase (VIR44). The insertion site nucleic acid sequence identifying the VIR44 gene in MUT44 is shown in Table 46.

Table 46. MUT44 Transposon Insertion Site (SEQ ID NO:62)

GGCTTAACGCCAGCTATGTCAACGCTGCGGTTATGCGGATTTTTCATGCCTCTGCGGCTAACAGAAA
 AAAGCCTTATGATAGCTATACTAATGGGGCTTTTACTCCGTTTGTACCCGATTCCGTGACCGGCGTC
 AGGGTCAAGTCACAAAATCATCACAATTTTCCGTCACCGGCGCTACAATCGACCGAAGTCACAATC
 TCAAATCAGAAGAGTATTGCTAATGAAAAACATCAACCCAACGCAGACCTCTGCCCTGGCAGGCATTA
 CAGAAACACTTCGACGAAAATGAAAGATGTCATCAGCGAGCTTTTCGCCAAAGATAGCGACCGTT
 TTTCTAAATTTTCCGCGACGTTTCGACGATCTGATGCTGGTGGACTTCTCCAAAACCGCATCACTGA
 AGAGACGCTGGCTAAACTGCAGGATCTGGCGAAAGAGACTGACCTGGCGGGCGCTATCAAGTCGATG
 TTCTCAGGTGAGAAGATCAACCGCACCGAAGACCGCGCGGTACTGCACGTCGCGCT

MUT45

A *Klebsiella* bacterial mutant (MUT45) was made by transposon insertion in a *Klebsiella* sp. wild-type strain. In the *Dictyostelium* growth assay, the mutated
 15 microorganism was less virulent compared to an isogenic bacterial strain. The nucleotide sequence immediately following the transposon insertion was cloned and identified as the gene encoding DNA methylase (VIR45). The insertion site nucleic acid sequence identifying the VIR45 gene in MUT45 is shown in Table 47.

Table 47. MUT45 Transposon Insertion Site (SEQ ID NO:63)

TGCTTCATCCGCATCTCCTTGAAATTTATTTGGTCTTAGGCGGACGGTAGAGCGCTAATAGCTCGTC
 CACCTTTTACGCGTACCACCGTTGCTGCTGATGCTGCGCCGACCTTCACAATATGCGTTTCTGCC
 GCGTTTTTATACCATTCTGCGTCAGCGGCGTGGTGGTTGAAATCAGCACCAGGATGCGCTTTT
 TCATCAGCGATTCCGCCCTTTGCGCCAGCAGTACCTGTTGTTCCAGGTTGAAACTGTTGGTGTGGTA
 GGCGGTAAAGTTTCGCCGTCGCCGTTAGCGGCGCATAGGGCGGATCGCAATACACCACTGTGCGGCTA
 TCCGCACGTTGCATGCACTCTTCGTAAGATTTCGAGTAAACTCGGCGTTTTCGCCCTTCTCGGCGA
 AATGATAGAGCTCAGCTTCGGGGAATAGGGCTTTTATAACGGCCAAACGGCACATTGAACTCGCC
 GCGCAG

MUT46

A *Klebsiella* bacterial mutant (MUT46) was made by transposon insertion in a *Klebsiella* sp. wild-type strain. In the *Dictyostelium* growth assay, the mutated microorganism was less virulent compared to an isogenic bacterial strain. The nucleotide sequence immediately following the transposon insertion was cloned and identified as the gene encoding a putative inner membrane protein (VIR46). The insertion site nucleic acid sequence identifying the VIR46 gene in MUT46 is shown in Table 48.

Table 48. MUT46 Transposon Insertion Site (SEQ ID NO:64)

TGTC AATGCGCAATTTGGTTAAATATGTCGGTATTGGCCTGCTGGTGATGGGGCTTGCCGCTGCGA TAACAGCGATTCAAAGCGCCAACCGTTGGCGCAGCAGCGGAGAGCAATGCCAGCGCCAGGCAATC AGCCTGCTGGATGGCAAGCTGAGCTTCACCTGCTGCGGGCATGGCCGACCAGAGCGGCAAAC TGG GTACCCAGGCGAACAATATGCACGTCTACTCTGACGCTACCGCCAGAAAGCGGTCATCGTCATCGT CGGCGACAGCACCAATGA
--

IV. SUITABLE TARGET PATHOGENS

Other *Pseudomonas* sp. and *Klebsiella* sp. and many other microbes, including gram-negative bacterial strains, are likely to include virulence genes encoding VIRX-related peptides or proteins having amino acid sequence identity or similarity to those identified herein. Suitable bacterial pathogens may include, but are not limited to, *Pneumococci* sp., *Klebsiella*, sp., *Pseudomonas*, e.g., *P. aeruginosa*, *Salmonella*, e.g., *Salmonella typhimurium*, *Legionella*, e.g., *Legionella pneumophila*, *Escherichia*, e.g., *Escherichia coli*, *Listeria*, e.g., *Listeria monocytogenes*, *Staphylococcus*, e.g., *Staphylococcus aureus*, *Streptococci* sp., *Vibrio*, e.g., *Vibrio cholerae*. Pathogenic mycobacteria of the present invention may include e.g., *Mycobacterium tuberculosis*. Pathogenic fungi of the present invention may include, e.g., *Candida albicans*. Pathogenic unicellular eukaryotic organisms of the present invention may include, e.g., *Leishmania donovani*.

Having identified VIRX genes according to the invention, it is possible to use the gene sequence to search for related genes or peptides in other microorganisms. This may be carried out by searching in existing databases, e.g., EMBL or GenBank. The levels of identity between gene sequences and levels of identity or similarity between, amino acid sequences can be calculated using known methods. In relation to the present invention, publicly available computer based methods for determining identity and similarity include the BLASTP, BLASTN and FASTA (Atschul *et al.*, J. Molec. Biol., 1990; 215:403-410), the

BLASTX program available from NCBI, and the Gap program from Genetics Computer Group, Madison WI.

Preferably, the peptides that may be useful in the various aspects of the invention have greater than a 40% similarity with the peptides identified herein. More preferably, the peptides have greater than 60% sequence similarity. Most preferably, the peptides have greater than 80% sequence similarity, *e.g.*, 95% similarity. With regard to the polynucleotide sequences identified herein, related polynucleotides that may be useful in the various aspects of the invention may have greater than 40% identity with the sequences identified herein. More preferably, the polynucleotide sequences have greater than 60% sequence identity. Most preferably, the polynucleotide sequences have greater than 80% sequence identity, *e.g.*, 95% identity.

In addition to related molecules from other microorganisms, the invention encompasses modifications made to the peptides and polynucleotides identified herein which do not significantly alter the biological function. It will be apparent to the artisan that the degeneracy of the genetic code can result in polynucleotides with minor base changes from those specified herein, but which nevertheless encode the same peptides. Complementary polynucleotides are also within the invention. Conservative replacements at the amino acid level are also envisaged, *i.e.*, different acidic or basic amino acids may be substituted without substantial loss of function.

It is recognized in the art that highly refined mechanisms that regulate transcription have evolved and are present in bacteria. Most bacterial genes are organized into operons, which are groups of genes coding for related proteins. Operons can either be repressed or induced thus regulating those genes. An operon consists of an operator, promoter, regulator, and structural genes. The regulator gene codes for a repressor protein that binds to the operator, obstructing the promoter (thus, transcription) of the structural genes. The regulator does not have to be adjacent to other genes in the operon. If the repressor protein is removed, transcription may occur.

Transposon mutagenesis usually inactivates the gene in which the transposon is inserted, as well as any gene downstream in the same operon. If the VIRX gene is a structural gene in an operon, inactivation of the VIRX gene disrupts the expression of other structural genes in the same operon and positioned downstream of the inactivated VIRX gene. For example, an insertion in *pchE* gene also inactivates *pchF*, *pchG*, *pchH*, and *pchI* genes

because they all reside within the pchEFGHI operon and are downstream of the inactivated pchE gene. Accordingly, the present invention includes attenuation of virulence due to alteration of a VIRX gene residing in an operon as well as alterations to nucleic acid yielding loss of expression of structural genes located in the same operon and located downstream of the VIRX gene. In one embodiment, the present invention is an alteration inactivating the first gene of an operon carrying a VIRX gene of the invention. The alteration of nucleic acids of VIRX genes and VIRX-containing operons may be insertional inactivation or gene deletion. It is preferred that the alteration of nucleic acids of VIRX genes and VIRX-containing operons be insertional inactivation.

The present invention also provides for a bacterial strain comprising an operon encoding a gene selected from the group consisting of VIR1, VIR2, VIR3, VIR4, VIR5, VIR6, VIR7, VIR8, VIR9, VIR10, VIR11, VIR12, VIR13, VIR14, VIR15, VIR16, VIR17, VIR18, VIR19, VIR20, VIR21, VIR22, VIR23, VIR24, VIR25, VIR26, VIR27, VIR28, VIR29, VIR30, VIR31, VIR32, VIR33, VIR34, VIR35, VIR36, VIR37, VIR38, VIR39, VIR40, VIR41, VIR42, VIR44, VIR45, and VIR46, wherein the bacterial strain includes a mutation that reduces expression of the VIRX gene relative to an isogenic bacterial strain lacking the mutation. In one embodiment, the mutation reduces inhibition of *Dictyostelium* amoeba growth when compared to the growth of *Dictyostelium* amoeba in the presence of an isogenic bacterial strain lacking the mutation. In another embodiment, the attenuated bacterial strain has more than one mutation of an operon containing a VIRX gene when compared to an isogenic bacterial strain.

V. VIRX NUCLEIC ACIDS AND POLYPEPTIDES CAN BE USED TO IDENTIFY ANTIMICROBIAL DRUGS

A. Screening

In a separate embodiment, the VIRX genes, or their polynucleotide or polypeptide products disclosed herein is used in screening assays for the identification of potential antimicrobial drugs. Routine screening assays are known to those skilled in the art, and can be adapted using the VIRX products of the invention in the appropriate way. For example, the products of the invention can be used as the target for a potential drug, with the ability of the drug to inactivate or bind to the target indicating its potential antimicrobial activity. In the

methods of the present invention, one or more test compounds may be present or produced in the assay mixture. Preferably one compound is present, or produced, in the assay mixture.

B. Character of Antimicrobial Candidate Compositions

5 VIRX nucleic acids and polypeptides may be used to identify drugs or therapeutics in a candidate composition useful in the prevention or treatment of pathogen-associated disease or infection. A candidate composition can include one or more molecules for analysis in a screening assay and can be a synthetic or semi-synthetic molecules. Such molecules include inorganic as well as organic chemical molecules. The molecules may be less than about 500
10 Daltons or more than 500 Daltons. The molecules may be naturally occurring. Naturally occurring molecules may include, *e.g.*, saccharides, lipids, peptides, proteins, nucleic acids, or combinations thereof, *e.g.*, aminoglycosides, glycolipids, lipopolysaccharides, or macrolides. Proteins may be immunoglobulins, *e.g.*, polyclonal or monoclonal antibodies. Nucleic acids may be DNA or RNA, *e.g.*, small interfering RNA (siRNA). The precise source of the
15 molecule is not critical to the method of the present invention. The molecule might be derived from *e.g.*, synthetic compounds libraries that are commercially available, *e.g.*, Sigma-Aldrich (Milwaukee, WI), or libraries of natural occurring molecules in the form of bacterial, fungal, plant, and animal extracts such as those available from Xenova (Slough, UK). The synthetic (or semi-synthetic) or natural occurring molecules might be modified using standard
20 chemical, physical, or biochemical methods known in the art.

VI. VIRX NUCLEIC ACIDS AND POLYPEPTIDES CAN BE USED TO DETECT THE DEGREE OF VIRULENCE OF PATHOGENS

A diagnostic test can assist physicians in determining the type of disease and
25 appropriate associated therapy. As such, a separate embodiment of this invention provides for the use of VIRX genes or their polynucleotides or nucleic acid products as virulence markers for detecting the presence of a pathogen, a pathogen-associated disease, or the virulence of a pathogen. There are many diagnostic assay approaches known to the artisan. Generally, the diagnostic method used would comprise the steps of (a) obtaining a sample
30 from a potentially diseased subject or a diseased subject; (b) measuring the level of at least one polypeptide or polynucleotide virulence marker in the sample; and (c) comparing the amount of the virulence marker in the sample of step (a) to the amount of the virulence

marker present in a control sample from a second subject known not to have the presence of the pathogen, where an alteration in the expression level of the virulence marker in the first subject as compared to the control sample indicates the presence of a pathogen, a pathogen-associated disease, or the virulence of a pathogen. Preferably, the subject is a mammal. More preferred is that the subject is a human. The person of skill will recognize that diagnostic tests may be performed in an array-type format wherein, *e.g.*, the presence of two or more VIRX genes or gene products indicate the presence of a pathogen, a pathogen-associated disease, or the virulence of a pathogen.

10 **VII. ATTENUATED ORGANISMS OF THE PRESENT INVENTION CAN BE USED IN VACCINE PREPARATION**

In another embodiment, the invention provides for the use of the attenuated organisms described herein in vaccine preparation. The preparation of vaccines based on attenuated microorganisms is known to those skilled in the art. Vaccine compositions can be formulated with suitable carriers or adjuvants, *e.g.*, alum, as necessary or desired, to provide effective immunization against infection. The preparation of vaccine formulations will be apparent to the artisan. The attenuated microorganisms may be prepared with a mutation that disrupts the expression of any of the VIRX genes identified herein. The artisan will be aware of methods for disrupting expression of particular VIRX genes. Techniques that may be used include, but are not limited to, insertional inactivation, or gene deletion techniques. Attenuated microorganisms according to the invention may also comprise additional mutations in other genes, for example in a second gene identified herein or in a separate gene required for growth of the microorganism, *e.g.*, an *Aro* mutation. Attenuated microorganisms may also be used as carrier systems for the delivery of heterologous antigens, therapeutic proteins or nucleic acids (DNA or RNA). In this embodiment, the attenuated microorganisms are used to deliver a heterologous antigen, protein or nucleic acid to a particular site *in vivo*. Introduction of a heterologous antigen, peptide or nucleic acid into an attenuated microorganism can be carried out by conventional techniques, including the use of recombinant constructs, *e.g.*, vectors, which comprise polynucleotides that express the heterologous antigen or therapeutic protein, and also include suitable promoter sequences. Alternatively, the gene that encodes the heterologous antigen or protein may be incorporated into the genome of the organism and the endogenous promoters used to control expression. In the vaccines of the present invention, the pharmaceutically effective dosage of the mutants of the present invention to be

administered may vary depending on the age, weight and sex of the subject, and the mode of administration. The subject can be, *e.g.*, a human, a non-human primate (such as an ape, gorilla, or chimpanzee), cow, horse, pig, sheep, dog, cat, or rodent (including mouse or rat).

5 VIII. DEFINITIONS

As used herein, each of the following terms has the meaning associated with it in this section.

10 The term "pathogen," as used herein, is intended to include an agent that causes disease, especially a living microorganism such as a bacterium or fungus. The terms "agent" and "factor" are used interchangeably herein to describe pathogens or toxins useful in the methods of the present invention. Pathogens may include any bacteria, mycobacteria, fungi and unicellular eukaryotic organism, including wild types and mutants thereof, which causes disease or brings about damage or harm to a host organism. Pathogens may also be a poisonous substance, *e.g.*, toxin, which is produced by living cells or organisms and is
15 capable of causing disease when introduced to a host.

The term, "pathogenic," as used herein, is defined as an agent's ability to cause disease, damage or harm to a host organism.

The term, "attenuated," as used herein, means an organism made less virulent relative to an isogenic pathogenic organism.

20 The term, "virulence," as used herein, is a measure of the degree of pathogenicity of an agent to a host organism. Virulence is usually expressed as the dose of an agent or cell number of a pathogen that will elicit a pathological response in the host organism within a given time period. "Reducing the virulence" as used herein is defined as the ability of a compound to attenuate, diminish, decrease, suppress, or arrest the development of, or the
25 progression of disease, damage or harm to a host organism mediated by a pathogen.

The term, "host organism," as used herein, is intended to include any living organism. Preferably the host organism is a eukaryote, *e.g.*, vertebrate. More preferably the host organism is a mammal. It is most preferred that the host organism be a human.

30 The term, "mutant," as used herein, an organism carrying a specific mutation of a gene that is expressed in the organism's phenotype.

The term, "mutation," as used herein, is an alteration of one or more nucleic acids of a polynucleotide sequence encoding a gene. A mutation may include the insertion of additional nucleic acids to a polynucleotide sequence encoding a gene, e.g., insertional inactivation of a gene. Alternatively, a mutation may include, but is not limited to, deletion of one or more
5 nucleic acids of a polynucleotide sequence encoding a gene.

The term, "operon," as used herein, is a unit of bacterial gene expression and regulation comprising several genes usually with complementary functions. Typically an operon includes nucleic acid and control elements in the nucleic acid that may be recognized by regulators of gene products. Insertion in a gene in an operon interferes with the function
10 of this gene and of other genes located downstream or upstream in the operon. It is understood herein that the function attributed to a gene refers to its function and/or that of any gene located downstream or upstream in the same operon.

The term, "pharmaceutically effective dosage," as used herein, means that amount necessary at least partly to attain the desired effect, or to delay the onset of, inhibit the
15 progression of, or halt altogether, the onset or progression of the particular condition being treated.

The terms "similarity" and "identity" are known in the art. The use of the term "identity" refers to a sequence comparison based on identical matches between correspondingly identical positions in the sequences being compared. The term "similarity"
20 refers to a comparison between amino acid sequences, and takes into account not only identical amino acids in corresponding positions, but also functionally similar amino acids in corresponding positions. Thus similarity between polypeptide sequences indicates functional similarity, in addition to sequence similarity.

EQUIVALENTS

25 From the foregoing detailed description of the specific embodiments of the invention, it should be apparent that bacterial genes have been identified and assigned a new role in virulence. Further, these genes and their products are useful in the identification of antimicrobial agents, the diagnosis of pathogen-associated disease or infection as well as the preparation of vaccines. Although particular embodiments have been disclosed herein in
30 detail, this has been done by way of example for purposes of illustration only, and is not intended to be limiting with respect to the scope of the appended claims that follow. In particular, it is contemplated by the inventor that various substitutions, alterations, and

modifications may be made to the invention without departing from the spirit and scope of the invention as defined by the claims. For instance, the choice of the particular pathogen, or combination of pathogens selected for assay or vaccination, the test conditions used in diagnostic assays utilizing the pathogens of this invention, or the method of mutagenesis used to derive the attenuated mutants is believed to be a matter of routine for a person of ordinary skill in the art with knowledge of the embodiments described herein.

EXAMPLES

This Example is provided for the purpose of illustration only and the invention should in no way be construed as being limited to these Example, but rather should be construed to encompass any and all variations which become evident as a result of the teaching provided.

EXAMPLE 1 STRAINS AND CULTURE CONDITIONS USED TO SCREEN FOR ATTENUATED VIRULENCE IN TEST BACTERIAL MUTANTS.

The *D. discoideum* wild-type strain DH1-10 used in these studies is a subclone of DH1 (Cornillon *et al.*, J. Biol. Chem., 275(44):34287-92, 2000). Cells were grown at 21°C in HL5 medium (14.3 g/l peptone (Oxoid), 7.15 g/l yeast extract, 18g/l maltose, 0.64 g/l Na₂HPO₄·2H₂O, 0.49 g/l KH₂PO₄, pH 6.7) (Cornillon *et al.*, J. Cell. Sci., 107 (Pt 10):2691-704, 1994) and subcultured twice a week.

Bacteria were grown overnight at 37°C on Luria-Bertani (LB) agar. Single colonies were inoculated into 5 ml PB (2% (wt/vol) peptone, 0.3% (wt/vol) MgCl₂·6H₂O, 1% (wt/vol) K₂SO₄) (Essar *et al.*, J. Bacteriol., 172(2):884-900,1990) in a 50 ml flask and grown at 37°C for 8 hr prior to use. The growth of various strains was tested in rich medium (PB) by measuring the optical density (600 nm) of a culture at different times after inoculation and was found to be comparable for all strains used. Under these conditions, similar OD_{600s} were obtained for each strain and the induction of quorum sensing was maximal. Minimal Inhibitory Concentrations (MICs) were determined in Mueller-Hinton broth by the microdilution method (Thornsberry *et al.*, NCCLS, 3: 48-56, 1983). Mutations yielding reduced virulence were identified where the growth of the *Dictyostelium* test host organism exposed to the mutant pathogen was greater than the *Dictyostelium* test host organism exposed to wild-type pathogen. Specific genetic mutations in pathogens displaying reduced virulence were identified and characterized by techniques well know in the art.

CLAIMS

What is claimed is:

1. An attenuated bacterial mutant derived from a pathogenic bacterial strain, wherein said attenuated mutant has:

5 (i) a mutation of a gene selected from the group consisting of VIR1, VIR2, VIR3, VIR4, VIR5, VIR6, VIR7, VIR8, VIR9, VIR10, VIR11, VIR12, VIR13, VIR14, VIR15, VIR16, VIR17, VIR18, VIR19, VIR20, VIR21, VIR22, VIR23, VIR24, VIR25, VIR26, VIR27, VIR28, VIR29, VIR30, VIR31, VIR32, VIR33, VIR34, VIR35, VIR36, VIR37, VIR38, VIR39, VIR40, VIR41, VIR42, VIR43, VIR44, VIR45, and VIR46; and

10 (ii) reduced inhibition of *Dictyostelium* amoeba growth when compared to the growth observed in the presence of an isogenic bacterial strain.

2. An attenuated bacterial mutant of claim 1, wherein said mutation is insertional
15 inactivation or a gene deletion.

3. An attenuated bacterial mutant of claim 1, wherein said mutant is a gram-negative bacteria.

20 4. An attenuated bacterial mutant of claim 3, wherein said attenuated gram-negative bacterial mutant is a *Pseudomonas* species.

5. An attenuated bacterial mutant of claim 4, wherein said *Pseudomonas* species is *Pseudomonas aeruginosa*.

25 6. An attenuated *Pseudomonas* mutant of claim 5, wherein said attenuated *Pseudomonas* mutant is selected from the group consisting of: MUT1; MUT2; MUT3; MUT4; MUT5; MUT6; MUT7; MUT8; MUT9; MUT10; MUT11; MUT12; MUT13; MUT14; MUT15; MUT16; MUT17; MUT18; and MUT19.

7. An attenuated bacterial mutant of claim 3, wherein said gram-negative bacterial mutant is a *Klebsiella* species.

5 8. An attenuated bacterial mutant of claim 7, wherein said *Klebsiella* species is *Klebsiella pneumoniae*.

9. An attenuated *Klebsiella* mutant of claim 8, wherein said attenuated *Klebsiella* mutant is selected from the group consisting of: MUT20; MUT21; MUT22; MUT23;
10 MUT24; MUT25; MUT26; MUT27; MUT28; MUT29; MUT30; MUT31; MUT32; MUT33;
MUT34; MUT35; MUT36; MUT37; MUT38; MUT39; MUT40; MUT41; MUT42; MUT43;
MUT44; MUT45; and MUT46.

10. A method for identifying an antimicrobial drug, said method comprising:
15 (a) contacting a candidate composition with at least one polypeptide encoded by a gene selected from the group consisting of VIR1, VIR2, VIR3, VIR4, VIR5, VIR6, VIR7, VIR8, VIR9, VIR10, VIR11, VIR12, VIR13, VIR14, VIR15, VIR16, VIR17, VIR18, VIR19, VIR20, VIR21, VIR22, VIR23, VIR24, VIR25, VIR26, VIR27, VIR28, VIR29, VIR30, VIR31, VIR32, VIR33, VIR34, VIR35,
20 VIR36, VIR37, VIR38, VIR39, VIR40, VIR41, VIR42, VIR43, VIR44, VIR45 and VIR46; and
(b) comparing the biological activity of said polypeptide in the presence and absence of said candidate composition, wherein alteration of the biological activity of said polypeptide indicates that said candidate composition is an
25 antimicrobial drug.

11. A method of claim 10, wherein said candidate composition contains at least two molecules.

12. A method of claim 10, wherein said candidate composition contains at least one molecule less than about 500 Daltons.

13. A method of claim 10, wherein said candidate composition contains at least
5 one molecule greater than about 500 Daltons.

14. A method of claim 10, wherein said candidate composition contains at least one molecule selected from a group consisting of a polypeptide, polysaccharide, lipid, nucleic acid, or combination thereof.

10

15. A composition of claim 14, wherein said polypeptide is an immunoglobulin.

16. A method for identifying an antimicrobial drug, said method comprising:

15 (a) contacting a candidate composition with at least one polynucleotide encoded by a gene selected from the group consisting of VIR1, VIR2, VIR3, VIR4, VIR5, VIR6, VIR7, VIR8, VIR9, VIR10, VIR11, VIR12, VIR13, VIR14, VIR15, VIR16, VIR17, VIR18, VIR19, VIR20, VIR21, VIR22, VIR23, VIR24, VIR25, VIR26, VIR27, VIR28, VIR29, VIR30, VIR31, VIR32, VIR33, VIR34, VIR35, VIR36, VIR37, VIR38, VIR39, VIR40, VIR41, VIR42, VIR43, VIR44, VIR45, and
20 VIR46; and

(b) comparing the expression of said polynucleotide in the presence and absence of said candidate composition, wherein alteration of the expression of said nucleotide indicates that said candidate composition is an antimicrobial drug.

25 17. A method of claim 16, wherein said candidate composition contains at least two molecules.

18. A method of claim 16, wherein said candidate composition contains at least one molecule less than about 500 Daltons.

19. A method of claim 16, wherein said candidate composition contains at least one molecule greater than about 500 Daltons.

5 20. A method of claim 16, wherein said candidate composition contains at least one molecule selected from a group consisting of a polypeptide, polysaccharide, lipid, nucleic acid, or combination thereof.

21. A composition of claim 20, wherein said nucleic acid is a ribonucleic acid.

10

22. A nucleic acid of claim 21, wherein said nucleic acid is a small interfering ribonucleic acid.

23. A method for determining the degree of virulence of a pathogen in a subject,
15 said method comprising:

(a) measuring the level of expression of at least one polypeptide encoded by a gene selected from the group consisting of VIR1, VIR2, VIR3, VIR4, VIR5, VIR6, VIR7, VIR8, VIR9, VIR10, VIR11, VIR12, VIR13, VIR14, VIR15, VIR16, VIR17, VIR18, VIR19, VIR20, VIR21, VIR22, VIR23, VIR24, VIR25, VIR26,
20 VIR27, VIR28, VIR29, VIR30, VIR31, VIR32, VIR33, VIR34, VIR35, VIR36, VIR37, VIR38, VIR39, VIR40, VIR41, VIR42, VIR43, VIR44, VIR45, and VIR46, in a sample from the first subject; and

(b) comparing the amount of said polypeptide in said sample of step (a) to the amount of said polypeptide present in a control sample from a second subject
25 known not to have the presence of said pathogen, wherein an alteration in the expression level of said polypeptide in said first subject as compared to said control sample indicates the degree of virulence of said pathogen.

24. A method of claim 23, wherein said subject is a mammal.

25. A mammalian subject of claim 24, wherein said mammalian subject is a human.

5 26. A method for determining the degree of virulence of a pathogen in a subject, said method comprising:

(a) measuring the level of expression of at least one polynucleotide encoded by a gene selected from the group consisting of VIR1, VIR2, VIR3, VIR4, VIR5, VIR6, VIR7, VIR8, VIR9, VIR10, VIR11, VIR12, VIR13, VIR14, VIR15, VIR16, VIR17, VIR18, VIR19, VIR20, VIR21, VIR22, VIR23, VIR24, VIR25, VIR26, VIR27, VIR28, VIR29, VIR30, VIR31, VIR32, VIR33, VIR34, VIR35, VIR36, VIR37, VIR38, VIR39, VIR40, VIR41, VIR42, VIR44, VIR45, and VIR46, in a sample from the first subject; and

10 (b) comparing the amount of said polynucleotide in said sample of step (a) to the amount of said polynucleotide present in a control sample from a second subject known not to have the presence of said pathogen, wherein an alteration in the expression level of said polynucleotide in said first subject as compared to said control sample indicates the degree of virulence of said pathogen.

20 27. A method of claim 26, wherein said subject is a mammal.

28. A mammalian subject of claim 27, wherein said mammalian subject is a human.

25 29. An attenuated bacterial mutant of claim 1, wherein said mutant encodes and expresses a foreign antigen.

30. An attenuated bacterial mutant of claim 1, wherein said mutant contains a plasmid which encodes and expresses, in a eukaryotic cell, a foreign antigen.

31. A vaccine against a disease caused by a pathogenic microorganism comprising:

(a) a pharmaceutically effective dosage of one or more of the attenuated bacterial mutants of claim 1 and;

5 (b) a pharmaceutically acceptable diluent or carrier.

32. An attenuated bacterial mutant derived from a pathogenic bacterial strain, wherein said attenuated mutant has:

10 (i) a mutation of a gene selected from the group consisting of pchE, pchF, pchG, pchH, and pchI; and

(ii) reduced inhibition of *Dictyostelium* amoeba growth when compared to the growth observed in the presence of an isogenic bacterial strain.

33. A bacterial strain comprising an operon encoding a gene selected from the group consisting of VIR1, VIR2, VIR3, VIR4, VIR5, VIR6, VIR7, VIR8, VIR9, VIR10, VIR11, VIR12, VIR13, VIR14, VIR15, VIR16, VIR17, VIR18, VIR19, VIR20, VIR21, VIR22, VIR23, VIR24, VIR25, VIR26, VIR27, VIR28, VIR29, VIR30, VIR31, VIR32, VIR33, VIR34, VIR35, VIR36, VIR37, VIR38, VIR39, VIR40, VIR41, VIR42, VIR44, VIR45, and VIR46, wherein said bacterial strain includes a mutation that reduces expression of said gene relative to an isogenic bacterial strain lacking said mutation.

15
20

34. A bacterial strain of claim 33, wherein said mutation reduces inhibition of *Dictyostelium* amoeba growth when compared to the growth of *Dictyostelium* amoeba in the presence of an isogenic bacterial strain lacking said mutation.

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aaccagcgtc ccgagctgtg gaacatctac aacggcaagg tgaagaagg cgagtcgatc      540
cgcgctttcc cgctgtccaa ctggaccgag ctggacatct ggcaatacat ctacctggaa      600
ggcatccccg tcgtcccgtg gtacttcgcc gccgagcgcg aggtcatcga gaagaatggc      660
acattgatca tgatcgacga cgagcgcata ctcgagcata tctctgacga agagaaagcc      720
cgcatcgaga agcgcattgt gcgcttcctg accctcggct gctaccgct caccggcgcg      780
gtcgagtcca gcgccaccac gctgccggaa atcatccagg aaatgtctct gacgcgtact      840
tccgaacgcc agggccgggt catcgaccat gaccaggccg gttcgatgga agaaaagaaa      900
cgtcagggct atttctga

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918

09743PC.ST25.txt

<210> 4
 <211> 305
 <212> PRT
 <213> Pseudomonas aeruginosa

<400> 4

Met Val Asp Lys Leu Thr His Leu Lys Gln Leu Glu Ala Glu Ser Ile
 1 5 10 15

His Ile Ile Arg Glu Val Ala Ala Glu Phe Asp Asn Pro Val Met Leu
 20 25 30

Tyr Ser Ile Gly Lys Asp Ser Ala Val Met Leu His Leu Ala Arg Lys
 35 40 45

Ala Phe Phe Pro Gly Lys Leu Pro Phe Pro Val Met His Val Asp Thr
 50 55 60

Arg Trp Lys Phe Gln Glu Met Tyr Arg Phe Arg Asp Arg Met Val Glu
 65 70 75 80

Glu Met Gly Leu Asp Leu Ile Thr His Val Asn Pro Asp Gly Val Ala
 85 90 95

Gln Gly Ile Asn Pro Phe Thr His Gly Ser Ala Lys His Thr Asp Val
 100 105 110

Met Lys Thr Glu Gly Leu Lys Gln Ala Leu Asp Lys Tyr Gly Phe Asp
 115 120 125

Ala Ala Phe Gly Gly Ala Arg Arg Asp Glu Glu Lys Ser Arg Ala Lys
 130 135 140

Glu Arg Val Tyr Ser Phe Arg Asp Ser Lys His Arg Trp Asp Pro Lys
 145 150 155 160

Asn Gln Arg Pro Glu Leu Trp Asn Ile Tyr Asn Gly Lys Val Lys Lys
 165 170 175

Gly Glu Ser Ile Arg Val Phe Pro Leu Ser Asn Trp Thr Glu Leu Asp
 180 185 190

Ile Trp Gln Tyr Ile Tyr Leu Glu Gly Ile Pro Ile Val Pro Leu Tyr
 195 200 205

Phe Ala Ala Glu Arg Glu Val Ile Glu Lys Asn Gly Thr Leu Ile Met
 210 215 220

Ile Asp Asp Glu Arg Ile Leu Glu His Leu Ser Asp Glu Glu Lys Ala

09743PC.ST25.txt

225

230

235

240

Arg Ile Glu Lys Arg Met Val Arg Phe Arg Thr Leu Gly Cys Tyr Pro
 245 250 255

Leu Thr Gly Ala Val Glu Ser Ser Ala Thr Thr Leu Pro Glu Ile Ile
 260 265 270

Gln Glu Met Leu Leu Thr Arg Thr Ser Glu Arg Gln Gly Arg Val Ile
 275 280 285

Asp His Asp Gln Ala Gly Ser Met Glu Glu Lys Lys Arg Gln Gly Tyr
 290 295 300

Phe
 305

<210> 5
 <211> 822
 <212> DNA
 <213> Pseudomonas aeruginosa

<400> 5
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 gccgcccacc tggccgcgca ccatatattg gaggcgggat tgcggggcgt ggcgccggac 180
 attccggtgc tttccgaaga ggattgcgag ataccgctga gcgagcgcg cactggcgcg 240
 cgctggtggc tgggtggacc gctggacggc accaaggagt tcatctccgg tagcgaggag 300
 ttcaccgtca acgtggccct ggtcgaggat ggccgggtgc tgttcggcct ggtcggcggtg 360
 ccggtgagcg gccgctgcta ctacggtggc gccggtctcg gtgcctggcg cgaggaggcc 420
 gatggccgcy cgcaaccgat cagtgtgcgc ctggagcccc aggaggcctt caccgtggtg 480
 gccagcaagc gccatggcag cccggcccag gagcgcctgc tggatggctt gagcgagcgc 540
 ttcggcgacc tgcggcgagc cagcatcggc agttcgctga agttctgcct gctggccgag 600
 ggcgctgccg actgctatcc gcgcctgacg ccaacctcgc aatgggacac ggccgcccgc 660
 cagggtgtgc tggaaggcgc cggcggcgag gtgctcgacc tgcattggtg gccattcacc 720
 tacgagccgc gcgaggatta cctcaacggc tccttcctgg ccctgccgcy cgccgcccag 780
 tggcgagcgc agctgatcca actggcgcg gcgctgcaact ga 822

<210> 6
 <211> 273
 <212> PRT
 <213> Pseudomonas aeruginosa

<400> 6

09743PC.ST25.txt

Met Arg Pro Val Pro Trp Gly Glu Leu Val Ala Leu Val Arg Arg Ala
 1 5 10 15
 Gly Glu Ala Ile Leu Pro His Trp Arg Ala Asp Val Val Val Arg Ser
 20 25 30
 Lys Ala Asp Glu Ser Pro Val Thr Ala Ala Asp Leu Ala Ala His His
 35 40 45
 Ile Leu Glu Ala Gly Leu Arg Ala Leu Ala Pro Asp Ile Pro Val Leu
 50 55 60
 Ser Glu Glu Asp Cys Glu Ile Pro Leu Ser Glu Arg Gly His Trp Arg
 65 70 75 80
 Arg Trp Trp Leu Val Asp Pro Leu Asp Gly Thr Lys Glu Phe Ile Ser
 85 90 95
 Gly Ser Glu Glu Phe Thr Val Asn Val Ala Leu Val Glu Asp Gly Arg
 100 105 110
 Val Leu Phe Gly Leu Val Gly Val Pro Val Ser Gly Arg Cys Tyr Tyr
 115 120 125
 Gly Gly Ala Gly Leu Gly Ala Trp Arg Glu Glu Ala Asp Gly Arg Ala
 130 135 140
 Gln Pro Ile Ser Val Arg Leu Glu Pro Glu Glu Ala Phe Thr Val Val
 145 150 155 160
 Ala Ser Lys Arg His Gly Ser Pro Ala Gln Glu Arg Leu Leu Asp Gly
 165 170 175
 Leu Ser Glu Arg Phe Gly Asp Leu Arg Arg Ala Ser Ile Gly Ser Ser
 180 185 190
 Leu Lys Phe Cys Leu Leu Ala Glu Gly Ala Ala Asp Cys Tyr Pro Arg
 195 200 205
 Leu Thr Pro Thr Ser Gln Trp Asp Thr Ala Ala Ala Gln Gly Val Leu
 210 215 220
 Glu Gly Ala Gly Gly Glu Val Leu Asp Leu His Gly Ala Pro Phe Thr
 225 230 235 240
 Tyr Glu Pro Arg Glu Asp Tyr Leu Asn Gly Ser Phe Leu Ala Leu Pro
 245 250 255

09743PC.ST25.txt

Arg Ala Ala Glu Trp Arg Ser Glu Leu Ile Gln Leu Ala Arg Ala Leu
 260 265 270

His

<210> 7

<211> 1299

<212> DNA

<213> Pseudomonas aeruginosa

<400> 7

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atgcgagttc tggtccttgg cagcgggtgtc atcgggtaccg ccagtgcgta ttacctggcc      60
cgtgccgggt tgcaggtggt ggtgggtcgac cgtcaggacg gtcccgcgct ggaaaccagc      120
ttcgccaacg ccggccaggt gtctcccggc tacgcttcgc cctgggcagc cccgggcatt      180
cccctgaagg ccatgaagtg gctgctggaa aagcacgcgc cgctggccat caagctcacc      240
tccgatccca gccagtacgc ctggatgctg cagatgctgc gcaactgcac cgccgagcgc      300
tacgccgtga acaaggagcg catggtccgc ctgtccgagt acagccgcga ttgcctcgac      360
gaactgcgcg ccgagaccgg catcgccctac gagggccgca ccctcggcac cacccaactg      420
ttccgcaccc aggcgcagct ggacgccgcc ggcaaggaca tcgccgtgct cgagcgctcc      480
ggcgtgccct acgaggttct cgaccgcgac ggcatcgccc gcgtagagcc ggctttggcc      540
aaggtcgccg acaagctggt cggcgccttg cgccctgcca acgaccagac cggcgactgc      600
cagctgttca ccaccgcct ggcggaatg gccaaaggcc tgggcgtgga gttccgcttc      660
ggccagaaca tcgagcgctt ggacttcgcc ggcgaccgca tcaacggcgt gctggtcaac      720
ggcgaattgc tcaccgccga cactacgtg ctggccctgg gcagctactc gccgcaactg      780
ctcaagccgc tgggtatcaa ggctccggtc tatccgctga agggttattc gctgaccgtg      840
ccgatcacca acccgagat ggcgccgacc tcgaccatcc tcgacgagac ctacaaggtg      900
gcgatcaccg gcttcgacca gcgcacccgc gtcggcggca tggcggaat cgccggcttc      960
gacctgtcgc tgaacccgcg ccgccgcgag accctggaaa tgatcaccac cgacctctat     1020
cccgagggcg gcgatatcag ccaggcgacc ttctggaccg gcctgcgccc ggcgaccccg     1080
gatggcaccg cgatcgtcgg cgccaccgc taccgcaacc tgttctcaa taccggccac     1140
ggcaccctgg gttggaccat ggctgcggg tcgggtcgct acctggccga cctgatggcg     1200
aagaagcgcc cgcagatcag taccgaaggc ctggatattt cccgctacag caattccccg     1260
gagaacgcca agaatgccca tccagcgcca gcacactaa
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```

<210> 8

<211> 432

<212> PRT

<213> Pseudomonas aeruginosa

09743PC.ST25.txt

<400> 8

Met Arg Val Leu Val Leu Gly Ser Gly Val Ile Gly Thr Ala Ser Ala
 1 5 10 15

Tyr Tyr Leu Ala Arg Ala Gly Phe Glu Val Val Val Val Asp Arg Gln
 20 25 30

Asp Gly Pro Ala Leu Glu Thr Ser Phe Ala Asn Ala Gly Gln Val Ser
 35 40 45

Pro Gly Tyr Ala Ser Pro Trp Ala Ala Pro Gly Ile Pro Leu Lys Ala
 50 55 60

Met Lys Trp Leu Leu Glu Lys His Ala Pro Leu Ala Ile Lys Leu Thr
 65 70 75 80

Ser Asp Pro Ser Gln Tyr Ala Trp Met Leu Gln Met Leu Arg Asn Cys
 85 90 95

Thr Ala Glu Arg Tyr Ala Val Asn Lys Glu Arg Met Val Arg Leu Ser
 100 105 110

Glu Tyr Ser Arg Asp Cys Leu Asp Glu Leu Arg Ala Glu Thr Gly Ile
 115 120 125

Ala Tyr Glu Gly Arg Thr Leu Gly Thr Thr Gln Leu Phe Arg Thr Gln
 130 135 140

Ala Gln Leu Asp Ala Ala Gly Lys Asp Ile Ala Val Leu Glu Arg Ser
 145 150 155 160

Gly Val Pro Tyr Glu Val Leu Asp Arg Asp Gly Ile Ala Arg Val Glu
 165 170 175

Pro Ala Leu Ala Lys Val Ala Asp Lys Leu Val Gly Ala Leu Arg Leu
 180 185 190

Pro Asn Asp Gln Thr Gly Asp Cys Gln Leu Phe Thr Thr Arg Leu Ala
 195 200 205

Glu Met Ala Lys Gly Leu Gly Val Glu Phe Arg Phe Gly Gln Asn Ile
 210 215 220

Glu Arg Leu Asp Phe Ala Gly Asp Arg Ile Asn Gly Val Leu Val Asn
 225 230 235 240

Gly Glu Leu Leu Thr Ala Asp His Tyr Val Leu Ala Leu Gly Ser Tyr

09743PC.ST25.txt

245

250

255

Ser Pro Gln Leu Leu Lys Pro Leu Gly Ile Lys Ala Pro Val Tyr Pro
 260 265 270

Leu Lys Gly Tyr Ser Leu Thr Val Pro Ile Thr Asn Pro Glu Met Ala
 275 280 285

Pro Thr Ser Thr Ile Leu Asp Glu Thr Tyr Lys Val Ala Ile Thr Arg
 290 295 300

Phe Asp Gln Arg Ile Arg Val Gly Gly Met Ala Glu Ile Ala Gly Phe
 305 310 315 320

Asp Leu Ser Leu Asn Pro Arg Arg Arg Glu Thr Leu Glu Met Ile Thr
 325 330 335

Thr Asp Leu Tyr Pro Glu Gly Gly Asp Ile Ser Gln Ala Thr Phe Trp
 340 345 350

Thr Gly Leu Arg Pro Ala Thr Pro Asp Gly Thr Pro Ile Val Gly Ala
 355 360 365

Thr Arg Tyr Arg Asn Leu Phe Leu Asn Thr Gly His Gly Thr Leu Gly
 370 375 380

Trp Thr Met Ala Cys Gly Ser Gly Arg Tyr Leu Ala Asp Leu Met Ala
 385 390 395 400

Lys Lys Arg Pro Gln Ile Ser Thr Glu Gly Leu Asp Ile Ser Arg Tyr
 405 410 415

Ser Asn Ser Pro Glu Asn Ala Lys Asn Ala His Pro Ala Pro Ala His
 420 425 430

<210> 9

<211> 771

<212> DNA

<213> Pseudomonas aeruginosa

<400> 9

atggcactgg caaaacgcat catcccctgc ctcgacgtgg acaacggccg agtgggtcaag 60

ggcgtcaagt tcgagaacat ccgcgacgcc ggcgaccccg tcgagatcgc tcgccgctac 120

gacgagcagg gtgccgacga gatcaccttc ctcgatatca ccgccagcgt cgacggggcgc 180

gacaccaccc tgcataccgt cgagcgcgatg gctagccagg tgttcattcc gctgaccgtg 240

ggcggcgggc tacgcagcgt gcaggacatc cgcaacctgt tgaatgccgg cgcggaacaag 300

gtctcgatca acaccgccgc ggtgttcaac cccgagttcg tcggtgaggc cgccgaccgc 360

09743PC.ST25.txt

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ttcggctcgc agtgcacgt ggtcgccatc gacgcgaaga aggtttccgc cccgggcgag    420
gcgccgcgct gggaaatctt cacccatggc gggcgcaagc ccaccgggct ggatgccgtg    480
ctctggggcga agaagatgga agacttgggc gctggcgaga ttctcctgac cagcatggac    540
caggacggcg tgaagagcgg ttacgacctg ggcgtgacct gcgccatcag cgaggcgggtg    600
aacgtgccgg tgatcgcttc cggcggcgtc ggcaacctgg agcacctggc cgccggcatc    660
ctcgaggggca aggccgacgc ggtgctcgcg gcgagcatct tccacttcgg cgagtacacc    720
gtgccggaag ccaaggccta cctggccagc cgcggtatcg tggcgcgctg a              771

```

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<210> 10
<211> 256
<212> PRT
<213> Pseudomonas aeruginosa

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```

<400> 10

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Met Ala Leu Ala Lys Arg Ile Ile Pro Cys Leu Asp Val Asp Asn Gly
1          5          10          15

```

```

Arg Val Val Lys Gly Val Lys Phe Glu Asn Ile Arg Asp Ala Gly Asp
          20          25          30

```

```

Pro Val Glu Ile Ala Arg Arg Tyr Asp Glu Gln Gly Ala Asp Glu Ile
          35          40          45

```

```

Thr Phe Leu Asp Ile Thr Ala Ser Val Asp Gly Arg Asp Thr Thr Leu
          50          55          60

```

```

His Thr Val Glu Arg Met Ala Ser Gln Val Phe Ile Pro Leu Thr Val
65          70          75          80

```

```

Gly Gly Gly Val Arg Ser Val Gln Asp Ile Arg Asn Leu Leu Asn Ala
          85          90          95

```

```

Gly Ala Asp Lys Val Ser Ile Asn Thr Ala Ala Val Phe Asn Pro Glu
          100          105          110

```

```

Phe Val Gly Glu Ala Ala Asp Arg Phe Gly Ser Gln Cys Ile Val Val
          115          120          125

```

```

Ala Ile Asp Ala Lys Lys Val Ser Ala Pro Gly Glu Ala Pro Arg Trp
          130          135          140

```

```

Glu Ile Phe Thr His Gly Gly Arg Lys Pro Thr Gly Leu Asp Ala Val
145          150          155          160

```

```

Leu Trp Ala Lys Lys Met Glu Asp Leu Gly Ala Gly Glu Ile Leu Leu

```

09743PC.ST25.txt

165

170

175

Thr Ser Met Asp Gln Asp Gly Val Lys Ser Gly Tyr Asp Leu Gly Val
 180 185 190

Thr Arg Ala Ile Ser Glu Ala Val Asn Val Pro Val Ile Ala Ser Gly
 195 200 205

Gly Val Gly Asn Leu Glu His Leu Ala Ala Gly Ile Leu Glu Gly Lys
 210 215 220

Ala Asp Ala Val Leu Ala Ala Ser Ile Phe His Phe Gly Glu Tyr Thr
 225 230 235 240

Val Pro Glu Ala Lys Ala Tyr Leu Ala Ser Arg Gly Ile Val Val Arg
 245 250 255

<210> 11
 <211> 1035
 <212> DNA
 <213> Pseudomonas aeruginosa

<400> 11
 atgatcaagg tcggcatcgt tggcgggtacg gggtatacgg gcgtggaact gctgcgcctg 60
 ctggcgcagc atccgcaggc ccgggtggaa gtgatcactt cgcgttccga ggccgggggtg 120
 aaggtcgccg acatgtaccc gaacctgcga ggtcattatg acgacctgca gttcagcgtg 180
 ccggacgcgc agcgcctcgg cgcttgcgac gtggtgttct tcgccacgcc gcacggcgtg 240
 gcgcacgcgc tggctggcga actgctggac gccggggaccc gggtcacga tctgtccgct 300
 gacttccgcc tggcggacgc cgaggagtgg gcgcgctggt acggccagcc gcatggcgct 360
 ccggcgctgc tcgacgagc tgtctacggc ctgccggaag tgaaccgcga gaagatccgc 420
 caggcccgcc tgatcgccgt gccgggctgc taccgcagc cgacccagct gggcctgate 480
 ccgctgctgg aagccggcct ggccgacgcc tcgcggctga tcgccgattg caagtccggg 540
 gtcagcgggt ccggtcgggg cgccaagggt ggctcgctgt tctgcgaggc gggcgaaagc 600
 atgatggcct acgcggtcaa agggcatcgg catctcccgg aaatcagcca gggcctgcgt 660
 cgggcctccg gcggcgacgt cgggctgacg ttcgtaccgc acctgacgcc aatgatccgc 720
 ggtatccatg caaccctcta tgcccatgtc ggggatcgct cggtcgacct ccaggcggtg 780
 ttcgagaagc gctacgccga cgaacccttc gtcgacgtga tgccggccgg cagccatccg 840
 gagacccgca gcgtgcgtgg cgcaatgtc tgccgaatcg ccgtgcatcg ccccagggc 900
 ggcgacctgg tgggtggtgct gtcggtgatc gacaacctgg tcaagggcgc ctcgggtcag 960
 gcgctccaga acatgaacat cctgttcggg ctggacgagc gcctgggcct ctcgcatgcg 1020
 gccctgctcc cctga 1035

09743PC.ST25.txt

<210> 12
 <211> 344
 <212> PRT
 <213> Pseudomonas aeruginosa

<400> 12

Met Ile Lys Val Gly Ile Val Gly Gly Thr Gly Tyr Thr Gly Val Glu
 1 5 10 15

Leu Leu Arg Leu Leu Ala Gln His Pro Gln Ala Arg Val Glu Val Ile
 20 25 30

Thr Ser Arg Ser Glu Ala Gly Val Lys Val Ala Asp Met Tyr Pro Asn
 35 40 45

Leu Arg Gly His Tyr Asp Asp Leu Gln Phe Ser Val Pro Asp Ala Gln
 50 55 60

Arg Leu Gly Ala Cys Asp Val Val Phe Phe Ala Thr Pro His Gly Val
 65 70 75 80

Ala His Ala Leu Ala Gly Glu Leu Leu Asp Ala Gly Thr Arg Val Ile
 85 90 95

Asp Leu Ser Ala Asp Phe Arg Leu Ala Asp Ala Glu Glu Trp Ala Arg
 100 105 110

Trp Tyr Gly Gln Pro His Gly Ala Pro Ala Leu Leu Asp Glu Ala Val
 115 120 125

Tyr Gly Leu Pro Glu Val Asn Arg Glu Lys Ile Arg Gln Ala Arg Leu
 130 135 140

Ile Ala Val Pro Gly Cys Tyr Pro Thr Ala Thr Gln Leu Gly Leu Ile
 145 150 155 160

Pro Leu Leu Glu Ala Gly Leu Ala Asp Ala Ser Arg Leu Ile Ala Asp
 165 170 175

Cys Lys Ser Gly Val Ser Gly Ala Gly Arg Gly Ala Lys Val Gly Ser
 180 185 190

Leu Phe Cys Glu Ala Gly Glu Ser Met Met Ala Tyr Ala Val Lys Gly
 195 200 205

His Arg His Leu Pro Glu Ile Ser Gln Gly Leu Arg Arg Ala Ser Gly
 210 215 220

09743PC.ST25.txt

Gly Asp Val Gly Leu Thr Phe Val Pro His Leu Thr Pro Met Ile Arg
 225 230 235 240

Gly Ile His Ala Thr Leu Tyr Ala His Val Ala Asp Arg Ser Val Asp
 245 250 255

Leu Gln Ala Leu Phe Glu Lys Arg Tyr Ala Asp Glu Pro Phe Val Asp
 260 265 270

Val Met Pro Ala Gly Ser His Pro Glu Thr Arg Ser Val Arg Gly Ala
 275 280 285

Asn Val Cys Arg Ile Ala Val His Arg Pro Gln Gly Gly Asp Leu Val
 290 295 300

Val Val Leu Ser Val Ile Asp Asn Leu Val Lys Gly Ala Ser Gly Gln
 305 310 315 320

Ala Leu Gln Asn Met Asn Ile Leu Phe Gly Leu Asp Glu Arg Leu Gly
 325 330 335

Leu Ser His Ala Ala Leu Leu Pro
 340

<210> 13
 <211> 1644
 <212> DNA
 <213> Pseudomonas aeruginosa

<400> 13
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 aaggccagca tggaaatccc cagtcccaag gccggggtag tgaaaagcat caaggcgaag 180
 gtcggcgaca ccttgaaaga aggtgacgaa atcctcgagc tggaagtgga aggcggcgaa 240
 cagcctgccg aagccaaggc cgaggcagcg cccgccaac cggaagcgcc gaaagccgaa 300
 gcgcctgctc ccgccccgag cgagagcaag ccggccgccc ccgcccgggc cagcgtccag 360
 gacatcaagg tcccggacat cggctcggcc ggcaaggcca acgtcatcga agtgatggtc 420
 aaggccggcg acacggtcga ggccgaccag tcgctgatca ccctggaatc cgacaaggcc 480
 agcatggaga tcccctcgcc ggcctccggg gtggtggaaa gcgtctcgat caaggctcgtt 540
 gacgaagtcg gcaccggcga cctgatcctc aagctgaagg tggaaggcgc cgctccggca 600
 gccgaagagc aaccggcagc cgctccggcc caggccgcgg cggccgccc cgagcagaag 660
 cccgcccggg cggcccctgc gccagccaag gccgataccc cggctccggt cggcgcaccc 720
 agccgcgacg gcgccaaggc ccacgccggc ccggcggtgc gcatgctggc gcgcgagttc 780

09743PC.ST25.txt

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ggcgctcgagc tgagcgaagt gaaagccagc ggtcccaagg gtcgcatcct caaggaagac      840
gtccaggcct tcgtcaagga gcaactgcag cgcgcccaagt ccggcggtgc cggcgccacc      900
ggcggagccg gcatcccgcc gatcccgga gtcgacttca gcaagttcgg cgaagtggaa      960
gaagtggcga tgacccgcct gatgcaggtc ggcgccgcca acctgcatcg cagctggctg     1020
aacgtgccgc acgtgacca gttcgaccag tcggacatca ccgacatgga agccttccgc     1080
gttgcccaga aggccgcggc ggagaaggcc ggggtcaagc tgaccgtact gccgatcctg     1140
ctcaaggcct gcgcccacct gctcaaggaa ctgccggact tcaacagttc gctggcccc     1200
agcggcaagg cgctgatccg caagaagtac gtacacatcg gcttcgccgt ggacactccg     1260
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gccgaggccg ccgacctggc cgacaaggcc cgcaacaaga agctctcggc cgatgccatg     1380
cagggcgccct gcttcaccat ctccagtctc ggccacatcg gcggcaccgg cttcacgccc     1440
atcgtcaacg cgcgggaagt ggcgatcctc ggtgtgtcca aggcgaccat gcagccggta     1500
tgggacggca aggccttcca gccgcgcctg atgctgccgc tgtcgtgtc ctacgaccat     1560
cgcgtgatca acggtgccgc cgcggcgcg cttaccaagc gcctggggcga gctgctggcg     1620
gacatccgca ccctgctcct gtaa                                             1644

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<210> 14
 <211> 547
 <212> PRT
 <213> *Pseudomonas aeruginosa*

<400> 14

Met Ser Glu Leu Ile Arg Val Pro Asp Ile Gly Asn Gly Glu Gly Glu
 1 5 10 15

Val Ile Glu Leu Leu Val Lys Pro Gly Asp Lys Val Glu Ala Asp Gln
 20 25 30

Ser Leu Leu Thr Leu Glu Ser Asp Lys Ala Ser Met Glu Ile Pro Ser
 35 40 45

Pro Lys Ala Gly Val Val Lys Ser Ile Lys Ala Lys Val Gly Asp Thr
 50 55 60

Leu Lys Glu Gly Asp Glu Ile Leu Glu Leu Glu Val Glu Gly Gly Glu
 65 70 75 80

Gln Pro Ala Glu Ala Lys Ala Glu Ala Ala Pro Ala Gln Pro Glu Ala
 85 90 95

Pro Lys Ala Glu Ala Pro Ala Pro Ala Pro Ser Glu Ser Lys Pro Ala

09743PC.ST25.txt

100

105

110

Ala Pro Ala Ala Ala Ser Val Gln Asp Ile Lys Val Pro Asp Ile Gly
 115 120 125

Ser Ala Gly Lys Ala Asn Val Ile Glu Val Met Val Lys Ala Gly Asp
 130 135 140

Thr Val Glu Ala Asp Gln Ser Leu Ile Thr Leu Glu Ser Asp Lys Ala
 145 150 155 160

Ser Met Glu Ile Pro Ser Pro Ala Ser Gly Val Val Glu Ser Val Ser
 165 170 175

Ile Lys Val Gly Asp Glu Val Gly Thr Gly Asp Leu Ile Leu Lys Leu
 180 185 190

Lys Val Glu Gly Ala Ala Pro Ala Ala Glu Glu Gln Pro Ala Ala Ala
 195 200 205

Pro Ala Gln Ala Ala Ala Pro Ala Ala Glu Gln Lys Pro Ala Ala Ala
 210 215 220

Ala Pro Ala Pro Ala Lys Ala Asp Thr Pro Ala Pro Val Gly Ala Pro
 225 230 235 240

Ser Arg Asp Gly Ala Lys Val His Ala Gly Pro Ala Val Arg Met Leu
 245 250 255

Ala Arg Glu Phe Gly Val Glu Leu Ser Glu Val Lys Ala Ser Gly Pro
 260 265 270

Lys Gly Arg Ile Leu Lys Glu Asp Val Gln Val Phe Val Lys Glu Gln
 275 280 285

Leu Gln Arg Ala Lys Ser Gly Gly Ala Gly Ala Thr Gly Gly Ala Gly
 290 295 300

Ile Pro Pro Ile Pro Glu Val Asp Phe Ser Lys Phe Gly Glu Val Glu
 305 310 315 320

Glu Val Ala Met Thr Arg Leu Met Gln Val Gly Ala Ala Asn Leu His
 325 330 335

Arg Ser Trp Leu Asn Val Pro His Val Thr Gln Phe Asp Gln Ser Asp
 340 345 350

Ile Thr Asp Met Glu Ala Phe Arg Val Ala Gln Lys Ala Ala Ala Glu

09743PC.ST25.txt

355

360

365

Lys Ala Gly Val Lys Leu Thr Val Leu Pro Ile Leu Leu Lys Ala Cys
 370 375 380

Ala His Leu Leu Lys Glu Leu Pro Asp Phe Asn Ser Ser Leu Ala Pro
 385 390 395 400

Ser Gly Lys Ala Leu Ile Arg Lys Lys Tyr Val His Ile Gly Phe Ala
 405 410 415

Val Asp Thr Pro Asp Gly Leu Leu Val Pro Val Ile Arg Asp Val Asp
 420 425 430

Arg Lys Ser Leu Leu Gln Leu Ala Ala Glu Ala Ala Asp Leu Ala Asp
 435 440 445

Lys Ala Arg Asn Lys Lys Leu Ser Ala Asp Ala Met Gln Gly Ala Cys
 450 455 460

Phe Thr Ile Ser Ser Leu Gly His Ile Gly Gly Thr Gly Phe Thr Pro
 465 470 475 480

Ile Val Asn Ala Pro Glu Val Ala Ile Leu Gly Val Ser Lys Ala Thr
 485 490 495

Met Gln Pro Val Trp Asp Gly Lys Ala Phe Gln Pro Arg Leu Met Leu
 500 505 510

Pro Leu Ser Leu Ser Tyr Asp His Arg Val Ile Asn Gly Ala Ala Ala
 515 520 525

Ala Arg Phe Thr Lys Arg Leu Gly Glu Leu Leu Ala Asp Ile Arg Thr
 530 535 540

Leu Leu Leu
 545

<210> 15
 <211> 996
 <212> DNA
 <213> Pseudomonas aeruginosa

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09743PC.ST25.txt

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09743PC.ST25.txt

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His Arg His Pro Phe Asp Gln Pro Glu Ala Glu Gln Glu Leu Ala Asp
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09743PC.ST25.txt

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Leu Ala Glu Asp Asp His Val Leu Val Leu Val Gln His His Ile Val
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Ser Asp Gly Trp Ser Met Gln Val Met Val Glu Glu Leu Val Gln Leu
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Gly Glu Lys Glu Arg Gln Leu Ala Tyr Trp Thr Gly Leu Leu Gly Gly
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Ser Gln Ala Leu Arg Arg Val Ala Gln Gln Glu Gly Ala Thr Ala Phe

09743PC.ST25.txt

275

280

285

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530

535

09743PC.ST25.txt
540

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595 600 605

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Leu Ser Ala Asp Asn Leu Ala Tyr Val Ile Tyr Thr Ser Gly Ser Thr
645 650 655

Gly Lys Pro Lys Gly Thr Leu Leu Thr His Arg Asn Ala Leu Arg Leu
660 665 670

Phe Ser Ala Thr Glu Ala Trp Phe Gly Phe Asp Glu Arg Asp Val Trp
675 680 685

Thr Leu Phe His Ser Tyr Ala Phe Asp Phe Ser Val Trp Glu Ile Phe
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Gly Ala Leu Leu Tyr Gly Gly Cys Leu Val Ile Val Pro Gln Trp Val
705 710 715 720

Ser Arg Ser Pro Glu Asp Phe Tyr Arg Leu Leu Cys Arg Glu Gly Val
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Thr Val Leu Asn Gln Thr Pro Ser Ala Phe Lys Gln Leu Met Ala Val
740 745 750

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755 760 765

Ile Phe Gly Gly Glu Ala Leu Asp Leu Gln Ser Leu Arg Pro Trp Phe
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Gln Arg Phe Gly Asp Arg Gln Pro Gln Leu Val Asn Met Tyr Gly Ile

09743PC.ST25.txt
795

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09743PC.ST25.txt

1040

1045

1050

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Gln Leu Asp Ala Ser Leu Lys Ala Leu Phe Glu Arg Pro Val Leu
 1070 1075 1080

Glu Ala Phe Ala Gln Gly Leu Glu Arg Thr Thr Asp Ala Val Ser
 1085 1090 1095

Thr Ile Pro Leu Ala Asp Arg Gln Gln Pro Leu Ala Leu Ser Phe
 1100 1105 1110

Ala Gln Glu Arg Gln Trp Phe Leu Trp Gln Leu Glu Pro Glu Ser
 1115 1120 1125

Ala Ala Tyr His Ile Pro Ser Ala Leu Arg Leu Arg Gly Arg Leu
 1130 1135 1140

Asp Val Asp Ala Leu Gln Arg Ser Phe Asp Ser Leu Val Ala Arg
 1145 1150 1155

His Glu Thr Leu Arg Thr Arg Phe Arg Leu Glu Gly Gly Arg Ser
 1160 1165 1170

Tyr Gln Gln Val Gln Pro Ala Val Ser Val Ser Ile Glu Arg Glu
 1175 1180 1185

Gln Phe Gly Glu Glu Gly Leu Ile Glu Arg Ile Gln Ala Ile Val
 1190 1195 1200

Val Gln Pro Phe Asp Leu Glu Arg Gly Pro Leu Leu Arg Val Asn
 1205 1210 1215

Leu Leu Gln Leu Ala Glu Asp Asp His Val Leu Val Leu Val Gln
 1220 1225 1230

His His Ile Val Ser Asp Gly Trp Ser Met Gln Val Met Val Glu
 1235 1240 1245

Glu Leu Val Gln Leu Tyr Ala Ala Tyr Ser Gln Gly Leu Asp Val
 1250 1255 1260

Val Leu Pro Ala Leu Pro Ile Gln Tyr Ala Asp Tyr Ala Leu Trp
 1265 1270 1275

Gln Arg Ser Trp Met Glu Ala Gly Glu Lys Glu Arg Gln Leu Ala

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1280

1285

1290

Tyr Trp Thr Gly Leu Leu Gly Gly Glu Gln Pro Val Leu Glu Leu
 1295 1300 1305

Pro Phe Asp Arg Pro Arg Pro Ala Arg Gln Ser His Arg Gly Ala
 1310 1315 1320

Gln Leu Gly Phe Glu Leu Ser Arg Glu Leu Val Glu Ala Val Arg
 1325 1330 1335

Ala Leu Ala Gln Arg Glu Gly Ala Ser Ser Phe Met Leu Leu Leu
 1340 1345 1350

Ala Ser Phe Gln Ala Leu Leu Tyr Arg Tyr Ser Gly Gln Ala Asp
 1355 1360 1365

Ile Arg Val Gly Val Pro Ile Ala Asn Arg Asn Arg Val Glu Thr
 1370 1375 1380

Glu Arg Leu Ile Gly Phe Phe Val Asn Thr Gln Val Leu Lys Ala
 1385 1390 1395

Asp Leu Asp Gly Arg Met Gly Phe Asp Glu Leu Leu Ala Gln Ala
 1400 1405 1410

Arg Gln Arg Ala Leu Glu Ala Gln Ala His Gln Asp Leu Pro Phe
 1415 1420 1425

Glu Gln Leu Val Glu Ala Leu Gln Pro Glu Arg Asn Ala Ser His
 1430 1435 1440

Asn Pro Leu Phe Gln Val Leu Phe Asn His Gln Ser Glu Ile Arg
 1445 1450 1455

Ser Val Thr Pro Glu Val Gln Leu Glu Asp Leu Arg Leu Glu Gly
 1460 1465 1470

Leu Ala Trp Asp Gly Gln Thr Ala Gln Phe Asp Leu Thr Leu Asp
 1475 1480 1485

Ile Gln Glu Asp Glu Asn Gly Ile Trp Ala Ser Phe Asp Tyr Ala
 1490 1495 1500

Thr Asp Leu Phe Asp Ala Ser Thr Val Glu Arg Leu Ala Gly His
 1505 1510 1515

Trp Arg Asn Leu Leu Arg Gly Ile Val Ala Asn Pro Arg Gln Arg

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1520

1525

1530

Leu Gly Glu Leu Pro Leu Leu Asp Ala Pro Glu Arg Arg Gln Thr
 1535 1540 1545

Leu Ser Glu Trp Asn Pro Ala Gln Arg Glu Cys Ala Val Gln Gly
 1550 1555 1560

Thr Leu Gln Gln Arg Phe Glu Glu Gln Ala Arg Gln Arg Pro Gln
 1565 1570 1575

Ala Val Ala Leu Ile Leu Asp Glu Gln Arg Leu Ser Tyr Gly Glu
 1580 1585 1590

Leu Asn Ala Arg Ala Asn Arg Leu Ala His Cys Leu Ile Ala Arg
 1595 1600 1605

Gly Val Gly Ala Asp Val Pro Val Gly Leu Ala Leu Glu Arg Ser
 1610 1615 1620

Leu Asp Met Leu Val Gly Leu Leu Ala Ile Leu Lys Ala Gly Gly
 1625 1630 1635

Ala Tyr Leu Pro Leu Asp Pro Ala Ala Pro Glu Glu Arg Leu Ala
 1640 1645 1650

His Ile Leu Asp Asp Ser Gly Val Arg Leu Leu Leu Thr Gln Gly
 1655 1660 1665

His Leu Leu Glu Arg Leu Pro Arg Gln Ala Gly Val Glu Val Leu
 1670 1675 1680

Ala Ile Asp Gly Leu Val Leu Asp Gly Tyr Ala Glu Ser Asp Pro
 1685 1690 1695

Leu Pro Thr Leu Ser Ala Asp Asn Leu Ala Tyr Val Ile Tyr Thr
 1700 1705 1710

Ser Gly Ser Thr Gly Lys Pro Lys Gly Thr Leu Leu Thr His Arg
 1715 1720 1725

Asn Ala Leu Arg Leu Phe Ser Ala Thr Glu Ala Trp Phe Gly Phe
 1730 1735 1740

Asp Glu Arg Asp Val Trp Thr Leu Phe His Ser Tyr Ala Phe Asp
 1745 1750 1755

Phe Ser Val Trp Glu Ile Phe Gly Ala Leu Leu Tyr Gly Gly Arg

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1760

1765

1770

Leu Val Ile Val Pro Gln Trp Val Ser Arg Ser Pro Glu Asp Phe
 1775 1780 1785

Tyr Arg Leu Leu Cys Arg Glu Gly Val Thr Val Leu Asn Gln Thr
 1790 1795 1800

Pro Ser Ala Phe Lys Gln Leu Met Ala Val Ala Cys Ser Ala Asp
 1805 1810 1815

Met Ala Thr Gln Gln Pro Ala Leu Arg Tyr Val Ile Phe Gly Gly
 1820 1825 1830

Glu Ala Leu Asp Leu Gln Ser Leu Arg Pro Trp Phe Gln Arg Phe
 1835 1840 1845

Gly Asp Arg Gln Pro Gln Leu Val Asn Met Tyr Gly Ile Thr Glu
 1850 1855 1860

Thr Thr Val His Val Thr Tyr Arg Pro Val Ser Glu Ala Asp Leu
 1865 1870 1875

Lys Gly Gly Leu Val Ser Pro Ile Gly Gly Thr Ile Pro Asp Leu
 1880 1885 1890

Ser Trp Tyr Ile Leu Asp Arg Asp Leu Asn Pro Val Pro Arg Gly
 1895 1900 1905

Ala Val Gly Glu Leu Tyr Ile Gly Arg Ala Gly Leu Ala Arg Gly
 1910 1915 1920

Tyr Leu Arg Arg Pro Gly Leu Ser Ala Thr Arg Phe Val Pro Asn
 1925 1930 1935

Pro Phe Pro Gly Gly Ala Gly Glu Arg Leu Tyr Arg Thr Gly Asp
 1940 1945 1950

Leu Ala Arg Phe Gln Ala Asp Gly Asn Ile Glu Tyr Ile Gly Arg
 1955 1960 1965

Ile Asp His Gln Val Lys Val Arg Gly Phe Arg Ile Glu Leu Gly
 1970 1975 1980

Glu Ile Glu Ala Ala Leu Ala Gly Leu Ala Gly Val Arg Asp Ala
 1985 1990 1995

Val Val Leu Ala His Asp Gly Val Gly Gly Thr Gln Leu Val Gly

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2000

2005

2010

Tyr Val Val Ala Asp Ser Ala Glu Asp Ala Glu Arg Leu Arg Glu
 2015 2020 2025

Ser Leu Arg Glu Ser Leu Lys Arg His Leu Pro Asp Tyr Met Val
 2030 2035 2040

Pro Ala His Leu Met Leu Leu Glu Arg Met Pro Leu Thr Val Asn
 2045 2050 2055

Gly Lys Leu Asp Arg Gln Ala Leu Pro Gln Pro Asp Ala Ser Leu
 2060 2065 2070

Ser Gln Gln Ala Tyr Arg Ala Pro Gly Ser Glu Leu Glu Gln Arg
 2075 2080 2085

Ile Ala Ala Ile Trp Ala Glu Ile Leu Gly Val Glu Arg Val Gly
 2090 2095 2100

Leu Asp Asp Asn Phe Phe Glu Leu Gly Gly His Ser Leu Leu Leu
 2105 2110 2115

Leu Met Leu Lys Glu Arg Ile Gly Asp Thr Cys Gln Ala Thr Leu
 2120 2125 2130

Ser Ile Ser Gln Leu Met Thr His Ala Ser Val Ala Glu Gln Ala
 2135 2140 2145

Ala Cys Ile Glu Gly Gln Ala Arg Glu Ser Leu Leu Val Pro Leu
 2150 2155 2160

Asn Gly Arg Arg Glu Gly Ser Pro Leu Phe Met Phe His Pro Ser
 2165 2170 2175

Phe Gly Ser Val His Cys Tyr Lys Thr Leu Ala Met Ala Leu Arg
 2180 2185 2190

Asp Arg His Pro Val Lys Gly Val Val Cys Arg Ala Leu Leu Gly
 2195 2200 2205

Ala Gly Arg Glu Val Pro Glu Trp Asp Asp Met Val Ala Glu Tyr
 2210 2215 2220

Ala Glu Gln Leu Leu Gln Glu His Pro Glu Gly Val Phe Asn Leu
 2225 2230 2235

Ala Gly Trp Ser Leu Gly Gly Asn Leu Ala Met Asp Val Ala Ala

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2240

2245

2250

Arg Leu Glu Gln Arg Gly Arg Gln Val Ala Phe Val Gly Trp Ile
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Asp Ala Pro Ala Pro Val Arg Val Glu Ala Phe Trp Asn Glu Ile
 2270 2275 2280

Gly Pro Thr Pro Glu Ala Val Pro Asn Leu Ser Val Gly Glu Met
 2285 2290 2295

Arg Val Glu Leu Leu Gly Val Met Phe Pro Glu Arg Ala Glu His
 2300 2305 2310

Ile Glu Arg Ala Trp Ser Ser Ile Cys Ser Ala Thr Thr Asp Asp
 2315 2320 2325

Glu Gln Arg Trp Thr Arg Met Ser Asp Trp Ala Glu Ala Glu Ile
 2330 2335 2340

Gly Ala Glu Phe Ala Thr Leu Arg Ser Glu Ile Ala Gln Ser Asn
 2345 2350 2355

Glu Leu Glu Val Ser Trp Glu Leu Lys Gln Ile Leu Asp Glu Arg
 2360 2365 2370

Leu Lys Ala Met Asp Tyr Pro Arg Leu Thr Ala Lys Val Ser Leu
 2375 2380 2385

Trp Trp Ala Ala Arg Ser Thr Asn Ala Ile Gln Arg Ser Ala Val
 2390 2395 2400

Glu Arg Ser Met Ala Glu Ala Ile Gly Ala Glu Arg Val Glu Pro
 2405 2410 2415

Val Arg Val Leu Asp Thr Arg His Asp Lys Ile Ile Asp His Pro
 2420 2425 2430

Glu Phe Val Gln Ser Phe Arg Ala Ala Leu Glu Arg Ala Gly Arg
 2435 2440 2445

<210> 19

<211> 3132

<212> DNA

<213> Pseudomonas aeruginosa

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ctggccggcc tgctgggtcat ttccaaattg ccggtagcgc agtaccctaa tgcgcgccg 120

09743PC.ST25.txt

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09743PC.ST25.txt

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gccggggagt ga 3132

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<210> 20
 <211> 1043
 <212> PRT
 <213> *Pseudomonas aeruginosa*

<400> 20

Met Ser Glu Phe Phe Ile Lys Arg Pro Asn Phe Ala Trp Val Val Ala
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Leu Phe Ile Ser Leu Ala Gly Leu Leu Val Ile Ser Lys Leu Pro Val
 20 25 30

Ala Gln Tyr Pro Asn Val Ala Pro Pro Gln Ile Thr Ile Thr Ala Thr
 35 40 45

Tyr Pro Gly Ala Ser Ala Lys Val Leu Val Asp Ser Val Thr Ser Val
 50 55 60

Leu Glu Glu Ser Leu Asn Gly Ala Lys Gly Leu Leu Tyr Phe Glu Ser

65

75

80

Glu Asp Met Gln Tyr Ser Val Pro Tyr Asp Thr Ser Arg Phe Val Asp

09743PC.ST25.txt
330

325

335

Val Ala Ile Glu Lys Val Ile His Thr Leu Ile Glu Ala Met Val Leu
340 345 350

Val Phe Leu Val Met Phe Leu Phe Leu Gln Asn Val Arg Tyr Thr Leu
355 360 365

Ile Pro Ser Ile Val Val Pro Val Cys Leu Leu Gly Thr Leu Met Val
370 375 380

Met Tyr Leu Leu Gly Phe Ser Val Asn Met Met Thr Met Phe Gly Met
385 390 395 400

Val Leu Ala Ile Gly Ile Leu Val Asp Asp Ala Ile Val Val Val Glu
405 410 415

Asn Val Glu Arg Ile Met Ala Glu Glu Gly Ile Ser Pro Ala Glu Ala
420 425 430

Thr Val Lys Ala Met Lys Gln Val Ser Gly Ala Ile Val Gly Ile Thr
435 440 445

Leu Val Leu Ser Ala Val Phe Leu Pro Leu Ala Phe Met Ala Gly Ser
450 455 460

Val Gly Val Ile Tyr Gln Gln Phe Ser Val Ser Leu Ala Val Ser Ile
465 470 475 480

Leu Phe Ser Gly Phe Leu Ala Leu Thr Phe Thr Pro Ala Leu Cys Ala
485 490 495

Thr Leu Leu Lys Pro Ile Pro Glu Gly His His Glu Lys Arg Gly Phe
500 505 510

Phe Gly Ala Phe Asn Arg Gly Phe Ala Arg Val Thr Glu Arg Tyr Ser
515 520 525

Leu Leu Asn Ser Lys Leu Val Ala Arg Ala Gly Arg Phe Met Leu Val
530 535 540

Tyr Ala Gly Leu Val Ala Met Leu Gly Tyr Phe Tyr Leu Arg Leu Pro
545 550 555 560

Glu Ala Phe Val Pro Ala Glu Asp Leu Gly Tyr Met Val Val Asp Val
565 570 575

Gln Leu Pro Pro Gly Ala Ser Arg Val Arg Thr Asp Ala Thr Gly Glu

09743PC.ST25.txt

580

585

590

Glu Leu Glu Arg Phe Leu Lys Ser Arg Glu Ala Val Ala Ser Val Phe
 595 600 605

Leu Ile Ser Gly Phe Ser Phe Ser Gly Gln Gly Asp Asn Ala Ala Leu
 610 615 620

Ala Phe Pro Thr Phe Lys Asp Trp Ser Glu Arg Gly Ala Glu Gln Ser
 625 630 635 640

Ala Ala Ala Glu Ile Ala Ala Leu Asn Glu His Phe Ala Leu Pro Asp
 645 650 655

Asp Gly Thr Val Met Ala Val Ser Pro Pro Pro Ile Asn Gly Leu Gly
 660 665 670

Asn Ser Gly Gly Phe Ala Leu Arg Leu Met Asp Arg Ser Gly Val Gly
 675 680 685

Arg Glu Ala Leu Leu Gln Ala Arg Asp Thr Leu Leu Gly Glu Ile Gln
 690 695 700

Thr Asn Pro Lys Phe Leu Tyr Ala Met Met Glu Gly Leu Ala Glu Ala
 705 710 715 720

Pro Gln Leu Arg Leu Leu Ile Asp Arg Glu Lys Ala Arg Ala Leu Gly
 725 730 735

Val Ser Phe Glu Thr Ile Ser Gly Thr Leu Ser Ala Ala Phe Gly Ser
 740 745 750

Glu Val Ile Asn Asp Phe Thr Asn Ala Gly Arg Gln Gln Arg Val Val
 755 760 765

Ile Gln Ala Glu Gln Gly Asn Arg Met Thr Pro Glu Ser Val Leu Glu
 770 775 780

Leu Tyr Val Pro Asn Ala Ala Gly Asn Leu Val Pro Leu Ser Ala Phe
 785 790 795 800

Val Ser Val Lys Trp Glu Glu Gly Pro Val Gln Leu Val Arg Tyr Asn
 805 810 815

Gly Tyr Pro Ser Ile Arg Ile Val Gly Asp Ala Ala Pro Gly Phe Ser
 820 825 830

Thr Gly Glu Ala Met Ala Glu Met Glu Arg Leu Ala Ser Gln Leu Pro

09743PC.ST25.txt

835

840

845

Ala Gly Ile Gly Tyr Glu Trp Thr Gly Leu Ser Tyr Gln Glu Lys Val
 850 855 860

Ser Ala Gly Gln Ala Thr Ser Leu Phe Ala Leu Ala Ile Leu Val Val
 865 870 875 880

Phe Leu Leu Leu Val Ala Leu Tyr Glu Ser Trp Ser Ile Pro Leu Ser
 885 890 895

Val Met Leu Ile Val Pro Ile Gly Ala Ile Gly Ala Val Leu Ala Val
 900 905 910

Met Val Ser Gly Met Ser Asn Asp Val Tyr Phe Lys Val Gly Leu Ile
 915 920 925

Thr Ile Ile Gly Leu Ser Ala Lys Asn Ala Ile Leu Ile Val Glu Phe
 930 935 940

Ala Lys Glu Leu Trp Glu Gln Gly His Ser Leu Arg Asp Ala Ala Ile
 945 950 955 960

Glu Ala Ala Arg Leu Arg Phe Arg Pro Ile Ile Met Thr Ser Met Ala
 965 970 975

Phe Ile Leu Gly Val Ile Pro Leu Ala Leu Ala Ser Gly Ala Gly Ala
 980 985 990

Ala Ser Gln Arg Ala Ile Gly Thr Gly Val Ile Gly Gly Met Leu Ser
 995 1000 1005

Ala Thr Phe Leu Gly Val Leu Phe Val Pro Ile Cys Phe Val Trp
 1010 1015 1020

Leu Leu Ser Leu Leu Arg Ser Lys Pro Ala Pro Ile Glu Gln Ala
 1025 1030 1035

Ala Ser Ala Gly Glu
 1040

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 <211> 642
 <212> DNA
 <213> Pseudomonas aeruginosa

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09743PC.ST25.txt

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<210> 22
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 <212> PRT
 <213> *Pseudomonas aeruginosa*

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Arg Ala Met Leu Asp Ala Ala Thr Gln Ala Phe Leu Glu His Gly Phe
 20 25 30

Glu Gly Thr Thr Leu Asp Met Val Ile Glu Arg Ala Gly Gly Ser Arg
 35 40 45

Gly Thr Leu Tyr Ser Ser Phe Gly Gly Lys Glu Gly Leu Phe Ala Ala
 50 55 60

Val Ile Ala His Met Ile Gly Glu Ile Phe Asp Asp Ser Ala Asp Gln
 65 70 75 80

Pro Arg Pro Ala Ala Thr Leu Ser Ala Thr Leu Glu His Phe Gly Arg
 85 90 95

Arg Phe Leu Thr Ser Leu Leu Asp Pro Arg Cys Gln Ser Leu Tyr Arg
 100 105 110

Leu Val Val Ala Glu Ser Pro Arg Phe Pro Ala Ile Gly Lys Ser Phe
 115 120 125

Tyr Glu Gln Gly Pro Gln Gln Ser Tyr Leu Leu Leu Ser Glu Arg Leu
 130 135 140

Ala Ala Val Ala Pro His Met Asp Glu Glu Thr Leu Tyr Ala Val Ala

09743PC.ST25.txt
155

145

150

160

Cys Gln Phe Leu Glu Met Leu Lys Ala Asp Leu Phe Leu Lys Ala Leu
 165 170 175

Ser Val Ala Asp Phe Gln Pro Thr Met Ala Leu Leu Glu Thr Arg Leu
 180 185 190

Lys Leu Ser Val Asp Ile Ile Ala Cys Tyr Leu Glu His Leu Ser Gln
 195 200 205

Ser Pro Ala Gln Gly
 210

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 <212> DNA
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 <212> PRT
 <213> Pseudomonas aeruginosa

09743PC.ST25.txt

<400> 24

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Ala Glu Leu Ile Pro Ala Ser Ser Asp Ala Ser Phe Arg Arg Tyr Phe
 35 40 45

Arg Trp Gln Gly Gly Asp Arg Ser Leu Val Val Met Asp Ala Pro Pro
 50 55 60

Pro Gln Glu Asp Cys Arg Pro Phe Val Lys Val Ala Gly Leu Leu Ala
 65 70 75 80

Gly Ala Gly Val His Val Pro Arg Ile Leu Ala Gln Asp Leu Glu Asn
 85 90 95

Gly Phe Leu Leu Leu Ser Asp Leu Gly Arg Gln Thr Tyr Leu Asp Val
 100 105 110

Leu His Pro Gly Asn Ala Asp Glu Leu Phe Glu Pro Ala Leu Asp Ala
 115 120 125

Leu Ile Ala Phe Gln Lys Val Asp Val Ala Gly Val Leu Pro Ala Tyr
 130 135 140

Asp Glu Ala Val Leu Arg Arg Glu Leu Gln Leu Phe Pro Asp Trp Tyr
 145 150 155 160

Leu Ala Arg His Leu Gly Val Glu Leu Glu Gly Glu Thr Leu Ala Arg
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255

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425

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685

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725 730 735

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850 855 860

Gln Arg Phe Ala His Leu Lys Asp Pro Gln Thr Ala Tyr Arg Gln Leu
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Leu Gly Val Leu Gly His Pro Arg Val Phe Val His Arg Leu Glu Asp
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Trp Arg Lys Leu Ala Pro Ala Ala His Arg Ser Val Leu Gln Glu Ala
900 905 910

Glu Arg Gly Arg Gln Ala Val Ser Arg Thr Ala Leu Ser Cys Ile Asp
915 920 925

Pro Lys Leu Gln Ala Leu Glu Ala Asn Asp Trp Ala Val Val Leu Ser
Page 47

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940

930

935

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Glu Ala Leu Pro Leu Asp Ala Ala Ser Val Leu Tyr Val Leu Pro Ala
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Arg Met Thr Gln Gly Leu Lys Ile Ser Ala Gln Phe Glu Leu Asn
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<213> Pseudomonas aeruginosa

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<400> 30

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Glu Gln Leu Ala Asp Leu Leu Gly Glu Pro Leu Ala Asp Val Arg Ala
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Leu Ala Asp Asp Asp Asp Leu Leu Gly Cys Gly Leu Asp Ser Ile Arg
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Leu Met Tyr Leu Gln Glu Arg Leu Arg Ala Arg Gly Ser Thr Leu Asp
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09743PC.ST25.txt

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Leu Ala Cys Ala Asp Arg Leu Ser Ala Pro Ala Thr Val Ala Leu Pro
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 100 105 110

Ala Tyr Trp Leu Gly Arg Gly Ala Gly Glu Val Leu Gly Asn Val Ser
 115 120 125

Cys His Ala Phe Leu Glu Phe Arg Thr Arg Asp Val Asp Pro Gln Arg
 130 135 140

Leu Ala Ala Ala Ala Glu Cys Val Arg Gln Arg His Pro Met Leu Arg
 145 150 155 160

Ala Arg Phe Leu Asp Gly Arg Gln Gln Ile Leu Pro Thr Pro Pro Leu
 165 170 175

Ser Cys Phe Asp Leu Gln Asp Trp Arg Thr Leu Gln Val Asp Glu Ala
 180 185 190

Glu Arg Asp Trp Gln Ala Leu Arg Asp Trp Arg Ala His Glu Cys Leu
 195 200 205

Ala Val Glu Arg Gly Gln Val Phe Leu Leu Gly Leu Val Arg Met Pro
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Gly Gly Glu Asp Arg Leu Trp Leu Ser Leu Asp Leu Leu Ala Ala Asp
 225 230 235 240

Val Glu Ser Leu Arg Leu Leu Leu Ala Glu Leu Gly Val Ala Tyr Leu
 245 250 255

Ala Pro Glu Arg Leu Ala Glu Pro Pro Ala Leu His Phe Ala Asp Tyr
 260 265 270

Leu Ala His Arg Ala Ala Gln Arg Ala Glu Ala Ala Arg Ala Arg
 275 280 285

Asp Tyr Trp Leu Glu Arg Leu Pro Arg Leu Pro Asp Ala Pro Ala Leu
 290 295 300

Pro Leu Ala Cys Ala Pro Glu Ser Ile Arg Gln Pro Arg Thr Arg Arg
 305 310 315 320

09743PC.ST25.txt

Leu Ala Phe Gln Leu Ser Ala Gly Glu Ser Arg Arg Leu Glu Arg Leu
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Ala Ala Gln His Gly Val Thr Leu Ser Ser Val Phe Gly Cys Ala Phe
 340 345 350

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 355 360 365

Val Pro Leu Phe Asp Arg His Ala Asp Asp Pro Arg Ile Gly Glu Val
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Ile Ala Asp Phe Thr Thr Leu Leu Leu Leu Glu Cys Arg Met Gln Ala
 385 390 395 400

Gly Val Ser Phe Ala Glu Ala Val Lys Ser Phe Gln Arg Asn Leu His
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Asn Leu Gly Glu Glu Gly Phe Val Pro Ala Ala Phe Arg Asp Ala Phe
 450 455 460

Gly Asp Leu His Asp Met Leu Ser Gln Thr Pro Gln Val Trp Leu Asp
 465 470 475 480

His Gln Leu Tyr Arg Val Gly Asp Gly Ile Leu Leu Ala Trp Asp Ser
 485 490 495

Val Val Gly Leu Phe Pro Glu Gly Leu Pro Glu Thr Met Phe Glu Ala
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Tyr Val Gly Leu Leu Gln Arg Leu Cys Asp Ser Ala Trp Gly Gln Pro
 515 520 525

Ala Asp Leu Pro Leu Pro Trp Ala Gln Gln Ala Arg Arg Ala Leu Leu
 530 535 540

Asn Gly Gln Pro Ala Cys Ala Thr Ala Arg Thr Leu His Arg Asp Phe
 545 550 555 560

Phe Leu Arg Ala Ala Glu Ala Pro Asp Ala Asp Ala Leu Leu Tyr Arg
 565 570 575

09743PC.ST25.txt

Asp Gln Arg Val Thr Arg Gly Glu Leu Ala Glu Arg Ala Leu Arg Ile
 580 585 590

Ala Gly Gly Leu Arg Glu Ala Gly Val Arg Pro Gly Asp Ala Val Glu
 595 600 605

Val Ser Leu Pro Arg Gly Pro Gln Gln Val Ala Ala Val Phe Gly Val
 610 615 620

Leu Ala Ala Gly Ala Cys Tyr Val Pro Leu Asp Ile Asp Gln Pro Pro
 625 630 635 640

Ala Arg Arg Arg Leu Ile Glu Glu Ala Ala Gly Val Cys Leu Ala Ile
 645 650 655

Thr Glu Glu Asp Asp Pro Gln Ala Leu Pro Pro Arg Leu Asp Val Gln
 660 665 670

Arg Leu Leu Arg Gly Pro Ala Leu Ala Ala Pro Val Pro Leu Ala Pro
 675 680 685

Gln Ala Ser Ala Tyr Val Ile Tyr Thr Ser Gly Ser Thr Gly Val Pro
 690 695 700

Lys Gly Val Glu Val Ser His Ala Ala Ala Ile Asn Thr Ile Asp Ala
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Leu Leu Asp Leu Leu Arg Val Asn Ala Ser Asp Arg Leu Leu Ala Val
 725 730 735

Ser Ala Leu Asp Phe Asp Leu Ser Val Phe Asp Leu Phe Gly Gly Leu
 740 745 750

Gly Ala Gly Ala Ser Leu Val Leu Pro Ala Gln Glu Gln Ala Arg Asp
 755 760 765

Ala Ala Ala Trp Ala Glu Ala Ile Gln Arg His Ala Val Ser Leu Trp
 770 775 780

Asn Ser Ala Pro Ala Leu Leu Glu Met Ala Leu Ser Leu Pro Ala Ser
 785 790 795 800

Gln Ala Asp Tyr Arg Ser Leu Arg Ala Val Leu Leu Ser Gly Asp Trp
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Val Ala Leu Asp Leu Pro Gly Arg Leu Arg Pro Arg Cys Ala Glu Gly
 820 825 830

09743PC.ST25.txt

Cys Arg Leu His Val Leu Gly Gly Ala Thr Glu Ala Gly Ile Trp Ser
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 Asn Leu Gln Ser Val Asp Thr Val Pro Pro His Trp Arg Ser Ile Pro
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 Tyr Gly Arg Pro Leu Pro Gly Gln Ala Tyr Arg Val Val Asp Thr His
 865 870 875 880
 Gly Arg Asp Val Pro Asp Leu Val Val Gly Glu Leu Trp Ile Gly Gly
 885 890 895
 Ala Ser Leu Ala Arg Gly Tyr Arg Asn Asp Pro Glu Leu Ser Ala Arg
 900 905 910
 Arg Phe Val His Asp Ala Gln Gly Arg Trp Tyr Arg Thr Gly Asp Arg
 915 920 925
 Gly Arg Tyr Trp Gly Asp Gly Thr Leu Glu Phe Leu Gly Arg Val Asp
 930 935 940
 Gln Gln Val Lys Val Arg Gly Gln Arg Ile Glu Leu Gly Glu Val Glu
 945 950 955 960
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 965 970 975
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 995 1000 1005
 Ala Gly Leu Ala Glu Ala Glu Ala Val Leu Thr Arg Glu Ile Leu
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 Gly Ala Leu Leu Glu Ala Pro Leu Glu Leu Asp Asp Gly Leu Arg
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 Pro Ser Leu Asp Glu Ala Leu Arg Arg Leu Gly Trp Gln Ala Ala
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 Gly Leu Thr Ala Met Gly Asn Ala Leu Arg Gly Leu Leu Ala Gly
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09743PC.ST25.txt

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 Gln Ala Val Ala Ala Arg Leu Pro Asp Gly Arg Glu Ala Leu Ala
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 1175 1180 1185
 Glu His Leu Gly Arg Tyr Asp Arg Val Ile Ser Phe Ala Ala Leu
 1190 1195 1200
 His Ala Tyr Glu Ala Ser Arg Glu Gly Leu Ala Leu Ala Ala Ala
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 Glu Ser Pro Leu Ala Leu Leu Gly Ala Ala Leu Leu Asp Asp Arg
 1235 1240 1245
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 1265 1270 1275
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 Pro Glu Arg Leu Trp Cys Leu Pro Ser Leu Pro Leu Asn Gly Asn
 1310 1315 1320

09743PC.ST25.txt

Gly Lys Val Asp Arg Arg Arg Leu Ala Glu Ser Met Thr Arg Ala
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Leu Gly Glu Cys Arg His Glu Pro Ser Ala Glu Glu Pro Leu Glu
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Ala His Glu Gln Ala Leu Ala Glu Cys Trp Glu Ala Val Leu Lys
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Arg Pro Val Arg Arg Arg Glu Ala Ser Phe Phe Ser Leu Gly Gly
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Asp Ser Leu Leu Ala Thr Arg Leu Leu Ala Gly Ile Arg Glu Arg
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Phe Gly Val Arg Leu Gly Met Ala Asp Phe Tyr Arg Gln Pro Thr
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<213> Pseudomonas aeruginosa

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09743PC.ST25.txt

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09743PC.ST25.txt

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 35 40 45

Leu Glu His Leu Glu Gly Gly Pro Gly Trp Arg Ala Glu Pro Asp Met
 50 55 60

Ala His Gln Arg Phe Pro Leu Thr Pro Val Gln Ala Ala Tyr Val Leu
 65 70 75 80

Gly Arg Gln Ala Ala Phe Asp Tyr Gly Gly Asn Ala Cys Gln Leu Tyr
 85 90 95

Ala Glu Tyr Asp Trp Pro Ala Asp Thr Asp Pro Ala Arg Leu Glu Ala
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09743PC.ST25.txt

Ala Trp Asn Ala Met Val Glu Arg His Pro Met Leu Arg Ala Val Ile
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130 135 140

Leu Thr Val His Ala Cys Ala Gly Leu Asp Glu Ala Ala Phe Gln Ala
145 150 155 160

His Leu Glu Arg Val Arg Glu Arg Leu Asp His Ala Cys Ala Ala Leu
165 170 175

Asp Gln Trp Pro Val Leu Arg Pro Glu Leu Ser Ile Gly Arg Asp Ala
180 185 190

Cys Val Leu His Cys Ser Val Asp Phe Thr Leu Val Asp Tyr Ala Ser
195 200 205

Leu Gln Leu Leu Leu Gly Glu Trp Arg Arg Arg Tyr Leu Asp Pro Gln
210 215 220

Trp Thr Ala Glu Pro Leu Glu Ala Thr Phe Arg Asp Tyr Val Gly Val
225 230 235 240

Glu Gln Arg Arg Arg Gln Ser Pro Ala Trp Gln Arg Asp Arg Asp Trp
245 250 255

Trp Leu Ala Arg Leu Asp Ala Leu Pro Gly Arg Pro Asp Leu Pro Leu
260 265 270

Arg Val Gln Pro Asp Thr Arg Ser Thr Arg Phe Arg His Phe His Ala
275 280 285

Arg Leu Asp Glu Ala Ala Trp Gln Ala Leu Gly Ala Arg Ala Gly Glu
290 295 300

His Gly Leu Ser Ala Ala Gly Val Ala Leu Ala Ala Phe Ala Glu Thr
305 310 315 320

Ile Gly Arg Trp Ser Gln Ala Pro Ala Phe Cys Leu Asn Leu Thr Val
325 330 335

Leu Asn Arg Pro Pro Leu His Pro Gln Leu Ala Gln Val Leu Gly Asp
340 345 350

Phe Thr Ala Leu Ser Leu Leu Ala Val Asp Ser Arg His Gly Asp Ser
355 360 365

09743PC.ST25.txt

Phe Val Glu Arg Ala Arg Arg Ile Gly Glu Gln Met Phe Asp Asp Leu
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Asp His Pro Thr Phe Ser Gly Val Asp Leu Leu Arg Glu Leu Ala Arg
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Ile Gly Ser Val Gln Arg Leu Leu Gly Asp Gly Glu Ala Pro Arg Ala
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Pro Arg Tyr Met Ile Ser Gln Thr Pro Gln Val Trp Leu Asp Cys Gln
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Val Thr Asp Gln Phe Gly Gly Leu Glu Ile Gly Trp Asp Val Arg Leu
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Val Ala Gln His Ala Ser Ala Leu Arg Arg Val Leu Glu Ala His Gly
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Ala Gly Arg Gly Arg Arg Val Ala Val Met Leu Pro Lys Ser Ala Ala
 565 570 575

Gln Leu Val Ala Val Ile Gly Ile Leu Gln Ala Gly Ala Ala Tyr Val
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Pro Val Asp Ile Arg Gln Pro Pro Leu Arg Arg Gln Ala Ile Leu Ala
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Ser Ala Glu Val Val Ala Leu Val Cys Leu Glu Ser Asp Val Pro Asp
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09743PC.ST25.txt

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 675 680 685

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 690 695 700

Asp Leu Ser Val Tyr Asp Phe Phe Gly Ala Thr Ala Ala Gly Ala Gln
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Val Val Leu Pro Asp Pro Ala Arg Gly Ser Asp Pro Ser His Trp Ala
 725 730 735

Glu Leu Leu Glu Arg His Ala Ile Thr Leu Trp Asn Ser Val Pro Ala
 740 745 750

Gln Gly Gln Met Leu Ile Asp Tyr Leu Glu Ser Glu Pro Gln Arg His
 755 760 765

Leu Pro Gly Pro Arg Cys Val Leu Trp Ser Gly Asp Trp Ile Pro Val
 770 775 780

Ser Leu Pro Thr Arg Trp Trp Arg Arg Trp Pro Asp Ser Ala Leu Phe
 785 790 795 800

Ser Leu Gly Gly Ala Thr Glu Ala Ala Ile Trp Ser Ile Glu Gln Pro
 805 810 815

Ile Arg Pro Gln His Thr Glu Leu Ala Ser Ile Pro Tyr Gly Arg Ala
 820 825 830

Leu Arg Gly Gln Ser Val Glu Val Leu Asp Ala Arg Gly Arg Arg Cys
 835 840 845

Pro Pro Gly Val Arg Gly Glu Ile His Ile Gly Gly Val Gly Leu Ala
 850 855 860

Leu Gly Tyr Ala Gly Asp Pro Gln Arg Thr Ala Glu Arg Phe Val Arg
 865 870 875 880

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His Pro Asp Gly Arg Arg Leu Tyr Arg Thr Gly Asp Leu Gly Arg Tyr
 885 890 895

Leu Ala Asp Gly Ser Ile Glu Phe Leu Gly Arg Glu Asp Asp Gln Val
 900 905 910

Lys Ile Arg Gly His Arg Ile Glu Leu Ala Glu Leu Asp Ala Ala Leu
 915 920 925

Cys Ala His Pro Gln Val Asn Leu Ala Ala Thr Val Val Leu Gly Glu
 930 935 940

Thr His Glu Arg Ser Leu Ala Ser Phe Val Thr Leu His Ala Pro Val
 945 950 955 960

Glu Ala Gly Glu Asp Pro Arg Thr Ala Leu Asp Ala Val Arg Gln Arg
 965 970 975

Ala Ala Gln Ala Leu Arg Arg Asp Trp Gly Ser Glu Glu Gly Ile Ala
 980 985 990

Ala Ala Val Ala Ala Leu Asp Arg Ala Cys Leu Ala Ser Leu Ala Ala
 995 1000 1005

Trp Leu Ala Gly Ser Gly Leu Phe Ala Ser Ala Thr Pro Leu Asp
 1010 1015 1020

Leu Ala Thr Leu Cys Gln Arg Leu Gly Ile Ala Glu Ala Arg Gln
 1025 1030 1035

Arg Leu Leu Arg His Trp Leu Arg Gln Leu Glu Glu Gly Gly Tyr
 1040 1045 1050

Leu Arg Ala Glu Gly Glu Gly Trp Leu Gly Cys Ala Glu Arg Pro
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Ala Gln Ser Pro Glu Asp Ala Trp Thr Ala Phe Ala Gly Cys Ala
 1070 1075 1080

Pro Ala Ala Leu Trp Pro Ala Glu Leu Val Ala Tyr Leu Arg Asp
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Ser Ala Gln Ser Leu Gly Glu Gln Leu Ala Gly Arg Ile Ser Pro
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Ala Ala Leu Met Phe Pro Gln Gly Ser Ala Arg Ile Ala Glu Ala
 1115 1120 1125

09743PC.ST25.txt

Met Tyr Ser Gln Gly Leu His Ala Gln Ala Leu His Glu Ala Met
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 1160 1165 1170
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 1175 1180 1185
 Val Asp Tyr Leu Phe Thr Asp Val Ser Ser Tyr Phe Leu Ala Ala
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 Phe Asp Met Asn Gly Asp Leu Leu Asp Gln Gly Val Ala Pro His
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 Glu Trp Leu Ala Ala Gln Gly Gly Asp Leu Ala Cys Gly Val Val
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 Pro Pro Gly Ser Ala Leu Asp Leu Leu Gly Tyr Asp Val Leu Leu
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09743PC.ST25.txt

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 Leu Ile Ala Gln Leu Ile Ala Arg Leu Arg Glu Arg Leu Glu Ser
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 1460 1465 1470
 Gln Pro Thr Pro Arg Gly Leu Ala Glu Arg Leu Arg Ser Ala Pro
 1475 1480 1485
 Glu Glu Gly Arg Gly Pro Ala Leu Ala Ala Ala Arg Gly Val Ala
 1490 1495 1500
 Pro Ala Pro Ala Gly Met Ser Arg Ala Pro Leu Ala Glu Gly Ala
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 Val Ala Leu Asp Pro Leu Val Arg Leu Val Pro Gly Glu Gly Val
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 Pro Arg Val Leu Val His Glu Gly Leu Gly Thr Leu Leu Pro Tyr
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 Leu Ala Val His Asp Ser Asp Ala Tyr Leu Ala Ile Pro Ala Glu
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 His Leu Asn Ala Cys Leu Gly Arg Arg Tyr Ala Glu Ala Leu His
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 Arg Ala Gly Leu Arg Glu Val Asp Leu Leu Gly Tyr Cys Ser Gly
 1595 1600 1605

09743PC.ST25.txt

Gly Leu Val Ala Leu Glu Thr Ala Lys Ser Leu Val Gln Arg Gly
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 Tyr Arg Val Asp Asp Glu Arg Leu Leu Leu Phe Ser Phe Ala Ala
 1640 1645 1650
 Thr Leu Gly Leu Asp Thr Ala Ala Leu Gly Phe Pro Ala Pro Glu
 1655 1660 1665
 Arg Leu Gly Gln Ala Val Gln Ala Ala Leu Ala Gln Thr Pro Glu
 1670 1675 1680
 Arg Leu Val Ala Glu Ala Leu Ala Gly Leu Pro Gly Leu Ala Asp
 1685 1690 1695
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 Ala Asp Ala Val Ser Val Glu Arg Asp Thr Leu Tyr Arg Leu Phe
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 Cys His Ser Val Arg Ala Ser Gln Ala Glu Ala Pro Glu Pro Tyr
 1730 1735 1740
 Val Gly Ala Leu Arg Leu Phe Val Pro Asp Ala Gly Asn Pro Leu
 1745 1750 1755
 Val Pro Arg Tyr Ala Glu Ala Leu Glu Thr Gln Trp Arg Ala Ala
 1760 1765 1770
 Ala Leu Gly Ala Cys Gly Ile His Glu Val Pro Gly Gly His Phe
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<211> 1713

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<213> Pseudomonas aeruginosa

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09743PC.ST25.txt

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<211> 570

<212> PRT

<213> *Pseudomonas aeruginosa*

<400> 34

09743PC.ST25.txt

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 35 40 45
 Ala Gln Pro Ala Leu Leu Ala Leu Val Leu Leu Ala Val Leu Ala Trp
 50 55 60
 Leu Gly Cys Gln Ala Leu Ala Ala His Leu Ala His Arg Val Asp Ala
 65 70 75 80
 Asp Leu Cys Asn Asp Leu Arg Leu Arg Leu Leu Ala His Leu Gln Arg
 85 90 95
 Leu Pro Leu Asp Trp Phe Gly Arg Gln Gly Pro Asp Gly Val Ala Arg
 100 105 110
 Leu Val Glu Gln Asp Val Arg Ala Leu His Gln Leu Ile Ala His Ala
 115 120 125
 Pro Asn Asp Leu Ser Asn Leu Leu Val Val Pro Leu Val Ala Leu Leu
 130 135 140
 Trp Leu Ala Trp Leu His Pro Trp Leu Leu Leu Phe Cys Leu Leu Pro
 145 150 155 160
 Leu Val Leu Ala Ala Ala Gly Phe Leu Leu Leu Arg Ser Ala Arg Tyr
 165 170 175
 Arg Asp Leu Val Leu Arg Arg Asn Ala Ala Leu Glu Arg Leu Ser Ala
 180 185 190
 Asp Tyr Gly Glu Phe Ala His Asn Leu Leu Leu Ala Arg Gln Tyr Pro
 195 200 205
 Gly Ala Gly Ile Gln Gln Gly Ala Glu Ala Ser Ala Ala Ala Phe Gly
 210 215 220
 Glu Ala Phe Gly Ala Trp Val Lys Arg Val Gly His Leu Ala Ala Leu
 225 230 235 240
 Val Tyr Val Gln Leu Ser Thr Pro Trp Leu Leu Ala Trp Val Leu Leu
 245 250 255

09743PC.ST25.txt

Gly Ala Leu Ala Leu Asp Ala Leu Gly Val Pro Leu Ala Leu Gly Gln
 260 265 270

Ala Cys Ala Phe Leu Leu Leu Leu Arg Ala Leu Ala Ala Pro Val Gln
 275 280 285

Ala Leu Gly His Gly Gly Asp Ala Leu Leu Gly Ala Arg Ala Ala Ala
 290 295 300

Glu Arg Leu Gln Gln Val Phe Asp Gln Ala Pro Leu Ala Glu Gly Arg
 305 310 315 320

Ser Thr Arg Glu Pro Val Asp Gly Ala Val Ala Leu His Gly Leu Gly
 325 330 335

His Ala Tyr Glu Gly Val Glu Val Leu Ala Asp Ile Asp Leu Glu Leu
 340 345 350

Glu Asp Gly Ser Leu Val Ala Leu Val Gly Pro Ser Gly Ser Gly Lys
 355 360 365

Ser Thr Leu Leu His Leu Leu Ala Arg Tyr Met Asp Ala Gln Arg Gly
 370 375 380

Glu Leu Glu Val Gly Gly Leu Ala Leu Lys Asp Met Pro Asp Ala Val
 385 390 395 400

Arg His Arg His Ile Ala Leu Val Gly Gln Gln Ala Ala Ala Leu Glu
 405 410 415

Ile Ser Leu Ala Asp Asn Ile Ala Leu Phe Arg Pro Asp Ala Asp Leu
 420 425 430

Gln Glu Ile Arg Gln Ala Ala Arg Asp Ala Cys Leu Asp Glu Arg Ile
 435 440 445

Met Ala Leu Pro Arg Gly Tyr Asp Ser Val Pro Gly Arg Asp Leu Gln
 450 455 460

Leu Ser Gly Gly Glu Leu Gln Arg Leu Ala Leu Ala Arg Ala Leu Leu
 465 470 475 480

Ser Pro Ala Ser Leu Leu Leu Leu Asp Glu Pro Thr Ser Ala Leu Asp
 485 490 495

Pro Gln Thr Ala Arg Gln Val Leu Arg Asn Leu Arg Glu Arg Gly Gly
 500 505 510

09743PC.ST25.txt

Gly Arg Thr Arg Val Ile Val Ala His Arg Leu Ala Glu Val Ser Asp
 515 520 525

Ala Asp Leu Ile Leu Val Leu Val Ala Gly Arg Leu Val Glu Arg Gly
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Glu His Ala Ala Leu Leu Ala Ala Asp Gly Ala Tyr Ala Arg Leu Trp
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<211> 1725

<212> DNA

<213> Pseudomonas aeruginosa

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09743PC.ST25.txt

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<210> 36
<211> 574
<212> PRT
<213> Pseudomonas aeruginosa

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<400> 36

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Ala Ala Cys Gly Val Leu Leu Val Pro Leu Val Glu Ala Trp Phe Ala
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```

Glu Gly Ala Leu Pro Trp Arg Trp Val Ala Ala Leu Leu Gly Leu Ser
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```

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Leu Ala Gln Ala Leu Leu Gln Tyr Leu Ala Leu Arg Arg Gly Phe Ala
65           70           75           80

```

```

Ala Gly Gly Ser Leu Ala Ala Gly Leu Val Arg Ser Leu Val Ala Arg
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```

Leu Pro Arg Leu Ala Pro Pro Ala Leu Arg Arg Val Ala Pro Ala Glu
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Gly Leu Leu Arg Gly Pro Val Met Gln Ala Met Gly Ile Pro Ala His
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Leu Leu Gly Pro Leu Ile Ala Ala Leu Val Thr Pro Leu Gly Val Ile
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Leu Gly Leu Phe Leu Ile Asp Pro Ser Ile Ala Leu Gly Leu Leu Leu
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09743PC.ST25.txt

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 Arg Glu Ser Val Ala Arg Gln Gly Leu Glu Glu Ala Leu Arg Ser Leu
 210 215 220
 His Arg Ser Thr Leu Asp Leu Leu Arg Arg Ser Leu Pro Ser Gly Leu
 225 230 235 240
 Gly Phe Ala Leu Ala Val Gln Ala Ala Phe Ala Phe Ala Leu Leu Gly
 245 250 255
 Gly Ala Trp Ala Val Glu Arg Gln Trp Leu Asp Gly Ala Arg Leu Val
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 275 280 285
 Thr His Leu Asp Gln Ala Leu Arg Gly Ala Trp Gln Ala Leu Asp Thr
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 Glu Arg Pro His Asp Ala Ser Leu Ala Ala Glu Ala Val Glu Leu Arg
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 Pro Gly Ser Leu Asn Val Leu Val Gly Pro Ser Gly Ala Gly Lys Ser
 355 360 365
 Ser Leu Leu Ala Leu Leu Gly Arg Leu Tyr Asp Val Asp Ala Gly Arg
 370 375 380
 Val Leu Leu Gly Gly Val Asp Ile Arg Arg Leu Ser Glu Thr Thr Leu
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09743PC.ST25.txt

Ser Val Ala Trp Asn Leu Arg Met Ala Arg Ala Asp Ala Asp Leu Glu
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 465 470 475 480
 Ser Thr Ala Pro Leu Leu Leu Leu Asp Glu Pro Thr Ala Ser Leu Asp
 485 490 495
 Ala Ala Ser Glu Ala Gln Val Leu Arg Ser Leu Leu Gly Leu Arg Gly
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 Arg Arg Thr Leu Leu Val Val Thr His Arg Pro Ala Leu Ala Arg Gln
 515 520 525
 Ala Asp Gln Val Leu Leu Leu Glu Glu Gly Arg Leu Arg Leu Ser Gly
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09743PC.ST25.txt

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09743PC.ST25.txt

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<210> 39
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<212> DNA
<213> Klebsiella sp.

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gcgtatgtcc aacctgg 377

<210> 41
<211> 625
<212> DNA
<213> Klebsiella sp.

<400> 41
gccagcccc ctttcccgtc tgcccagtta aaagccttcg tggagcagga atttgctcag 60
attaagcatg ttctgcacgg catcagcctg ctgggtcagt gcccgacag cgtcaatgcc 120
gcgctgatct gccgcggcga aaagctctcc atcgccatca tggcgggtct gctggaagcc 180
cgtggacaca aagtcagtgt cattaaccgc gtcgaaaaac tgctcgccgt gggtcactat 240

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```

ctggaatcca ccgtcgatat cgccgaatcc acccgccgca ttgccgccag ccagatcccc 300
gcagaccata tgatcctgat ggccggggttt accgccggca atgagaaagg cgagctgggtg 360
gtgctggggc gtaacggctc cgactactcg gctgcggtac tggccgcctg cctgcgcgct 420
gactgctgcg aaatctggac cgatgtcgac ggagtgtaca cctgcgatcc gcgtcagggtg 480
ccggatgcgc gcctgctgaa atcgatgtct tatcaggagg cgatggagct ctccctacttt 540
ggcgcgaaaag tgctgcaccc gcgcaccatt gccctatcg ccagttcca aatcccatgc 600
ctgattaaaa ataccggcaa ccccc 625

```

<210> 42
 <211> 355
 <212> DNA
 <213> Klebsiella sp.

```

<400> 42
ggcgcagcgt ctgctcgtca ccgtcaagct cgaagcttaa cattgcgcca aaaccttttt 60
gctgacgcgc cgcaatttca tgcccctggt tttccggcag cgatggatga tacagctttt 120
tcaccagcgg ctgggttttc agatactcaa cgatcgccag ggcatttcgc tgcgccactt 180
ccatccgtgg agacagcgtc cgcagcccg cgaacagcag atagctgtcg aaggcgctgc 240
cggtgacgcc aatattattc gccaccatg ccagttcggg gacagttgcc ggatctttgg 300
caatcaccac cccggccacc acatcggagt gaccattgag gtatttggtg cagga 355

```

<210> 43
 <211> 500
 <212> DNA
 <213> Klebsiella sp.

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<400> 43
gttgcgtccc aggcgggtaa acgcatcctg caggtagtca atttcgtcgt cggccagcgc 60
cagaccaga cggaggttgg cgtcaatcag cgcctgacgc ccttcgcca gcaggtcgac 120
gctggtgacc ggcgtcggct gatggtgagc gaacagcttc tgcgccgctt ccagctcgtc 180
gaagacgctc tccatcatgc ggtcatgcag ctccgccgc accgcggccc actgcgcttc 240
ggtcaggggt gaggcttcaa cgtaatacgc cacgccgcgc tcaagacgca caacctgcgc 300
cagaccgcag ttgtgagcga tatcggtagc tttagaagac caggagaga tggtgccagg 360
gcgaggggtc acgagcagta atttaccggt cggggtatgg ctgcttaagc tcggggcata 420
ctgaagcagt cgcgccaggc gctcgcgatc gtcagcgctc agcggggcgt tcagatcggc 480
aaaatgaata tattcggcat 500

```

<210> 44
 <211> 439
 <212> DNA
 <213> Klebsiella sp.

09743PC.ST25.txt

<400> 44
gtattggcat cgtactcctg ggctggccgg tgacaaaggc gatgcgctta tctttgctgg 60
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gaataagtcg ggccggaaaa tcagcatagc gtgagtgcgg ggccaggaaa gagtcgtcga 180
aaccgcgggt cagtaaggcg tgcggatgaa gaatatggtg ttcataagacg .ccggaaatct 240
tttcggcgcg ggtctgcttg ggaatgccgt acagaatgtt cagcgcgggc tgaaccgccc 300
aacagacgaa cagcgctgaa gtgacgtgat ccttgGCCCA ctccagcacc tgtttgatct 360
gcggccagta agcaacatcg ttaaactcaa ccaggcctaa aggagcgccg gtaacaatca 420
ggcgtcaaa gttctgatc 439

<210> 45
<211> 297
<212> DNA
<213> *Klebsiella* sp.

<400> 45
gaggttcata tgtccgtact cgatctaaac gcgcttaatg cattgccgaa agtggaacgc 60
attctggcac tcgcggaaac caacgcccac ctggaaaagc ttgacgccga agggcgtgtg 120
gcgtgggccc tggaaaatct gccgggaaac tatgtgctgt cgtcgagctt tggcattcag 180
gcggcggtaa gtttgcatct ggtgaatcag atccgcccgg acattccggt gatcctcacc 240
gataccggct acctgttccc ggaaacctat cagttttattg acgagctgac ggacaag 297

<210> 46
<211> 502
<212> DNA
<213> *Klebsiella* sp.

<400> 46
tgttaaagcg tgcgttctac agcctgttag tcctgctcgg cctgctgctg ttgaccgtgc 60
tgggccttga ccgctggatg agctggaaaa ccgcgcccta tatctatgat gaactgcagg 120
acctgcccta ccgtcaggtc ggtgtggtgc tgggcaccgc caaatattac cgcaccggcg 180
tcataatca gtattaccgt taccgcatcc aggggtgcgt gaacgcctac aacagcggca 240
aggtcaacta tctcctgctg agcggcgata atgctctgca aagctacaat gaaccgatga 300
ccatgcgtcg ggacctgatt aaaggcggcg tcgatcccg gcgatatcgta ctggactatg 360
ccggtttccg taccctcgac tcgatcgctc gtaccgggaa agtgttcgac accaaccgact 420
tcattatcat caccagcgc ttccactgcg aacgggcgct gtttatcgcc ctgcatatgg 480
ggatccaggc ccagtgtac gc 502

<210> 47
<211> 500
<212> DNA

09743PC.ST25.txt

<213> Klebsiella sp.

<400> 47

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cgctgaacct cctcaaacia acgcaggccc tgcacctgtc ggctgcaggc gaccagcgtg      60
gatccgctca aacagctgca ggccgagcac cttctcaaag cgcgccagct cgcggctgac      120
cgtggggttg gaggtgtgca gcatccgcgc cgcttcgggtc aggttgccgg tggatcatcac      180
cgcgtgaaag atttcgatat gacgcaaatt gacggctggc atgcggtctc cgtgaggctc      240
ggctggaacc atatcatttt tgcataagat cgcgataaaa cgatattttt tattcgtctg      300
tcaactgtggc gtaatcagaa aaaacagcga ccaacacacg cactgcaccg gagttcttat      360
gccacactcg ctttacgcca ccgataactga cctgaccgcg gacaacctgc tgcgcctgcc      420
ggcggaattt ggctgcccgg tctgggtcta tgatgcgcag attattcgcc gccagatagc      480
ccagctcagc cagtttcgac                                     500
```

<210> 48

<211> 229

<212> DNA

<213> Klebsiella sp.

<400> 48

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ggcttcacc caaatcgctt tgcgggaac gatttttgc aaacggctt tgcattcttt      60
accctcttgc ccgctaagt cggtcactct gtcataaggc gcgccgctgc tgcagcacat      120
ccagtacctg ctgagcgta gctttcagat cttcatgccc gtgtaaacgc atcaatatgg      180
cgacgttggc ggcgacggcg gcttcgtgag cggcttcacc tttaccttg      229
```

<210> 49

<211> 466

<212> DNA

<213> Klebsiella sp.

<400> 49

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tggctcaacg ctgctcagtg gtgcgaggtg tcactttggt gatcacatcg gcgttgtctg      60
cacagtgaat tcagatccag cgcgcgctcc ggttttacgc acgtagtccg gattgtgggt      120
gcctttctta acgatattca gccacggccc ttcgagatgc aggccagcg cctgggtcgg      180
atgtttttgc agatattcgc gcatcacgcg cagcccttgc ttcacagat cgtcgtgga      240
ggtaatcagc gtcggcagga agctgggtgca gcctgagcgt tcgttggcct tctgcatgat      300
ctccagcgtt tcgacagtga ccgcctctgg gctgtcgtta aactgcacgc cgcgcagcc      360
gttgagctgg acgtcgataa aaccgggggc gattattgcg ccgttgactg agcgtgctc      420
gatgtcagac ggcaaactct ccagcggaca aagacgttcg ataaag      466
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<210> 50

<211> 450

<212> DNA

<213> Klebsiella sp.

09743PC.ST25.txt

<400> 50
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agctgatacc tttttccctg gctttttcca gcggcgatcg agaccataaa tatggtggat 120
atcgggggttg gctgagagca tatcccggtt ctcttcatac aacaggacat ccacgctggc 180
ggcgggggtac tgctgtttca gcgcgtgaat aagcggcgtg atcagcagca tgcgccatg 240
atggcgcagc ttaatgacca ggatccgcgc cgggttcaac gggccgcggg agagggtttc 300
aggcgtcata ctctgttctt catccaggat aagggttccg attctagggg atcagacaga 360
ttgagagaag cgttgtattg ctctaccatg acccgatacg tatggcctga ggacgttttc 420
gtgcacaatc ccgcaatttc tcatcacgat 450

<210> 51
<211> 450
<212> DNA
<213> Klebsiella sp.

<400> 51
cactcaggct tgctgtaac gcttggtcgc catcacgtaa ggctgtatcg aaaataatga 60
cttgctggct catggtttgg atccttagtc tgtgtcctgg cgccttggtg acgagcataa 120
aaaaacccgc gccaaaggcgc gggttttata gtcttgctgg aagatgactt aacgctgaac 180
gtcgcccaac agcctaccga gcaaatggca tgcgttttagt agtagtaggc tggtagatcg 240
agcgggtgca atcattgcgt caaactccag atgaaatcgt tatgctttta gagttactgg 300
atagccgttt taaagtcaac ccctggcatg gaaaaagcgt tttgggctga ctaaataaat 360
tagcaaaatg tgctgatgta agccccattt tgccgaagat cctatttttg accgaaggcg 420
gtttatcccc aatttgtttc atttgaaaaa 450

<210> 52
<211> 575
<212> DNA
<213> Klebsiella sp.

<400> 52
cgctgaaccg ctatccggag ccgcagccga agtgccgtga ttgagagcta cgcccgctac 60
gccgaggtca aaccggagca ggtgctggtc agccgcggcg ccgacgaagg catcgagctg 120
ctgatccgcg ccttctgtga gcccggcgaa gacgcggtgc tctactgccg gccgacctac 180
ggcatgtaca gcgtcagcgc cgagaccatc ggcgtcgagt gccgcaccgt gccgacgctg 240
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tttgtctgca gccgaacaa cccgaccggg cagattatcg acccgcagtc gatgcgcgac 360
ctgctggaga tgaccgcgg caaagccatc gtggtggccg acgaagccta tattgaattc 420
tgcccgagg cgacgctcgc cggctggctc agcgactatc cgcacctggt ggtgctgcgc 480

09743PC.ST25.txt

acgctgtcca aagccttcgc cctcgccggc ctgcgctgcg gcttcaccct cgccaacgcc 540

gaggtgatta acgtgctgct gaaagtgatc gcccc 575

<210> 53

<211> 375

<212> DNA

<213> Klebsiella sp.

<400> 53

cgtatatttc atcgtagaca aaccgtaa acaggcattg gctgattttc agtgagtga 60

tttaaataga cttctgccgt tttcaatgct tcggcgatgg tcacatccat atcaaggtaa 120

cggtagggtc caagacgacc gacaaaagtg atgttggttt cattctcggc caatgacaaa 180

tatttttcaa gaagagccat ttctcccatc tggcgaatag gatagtaagg aatatcattt 240

tcttcacaag cacggctata ctctttataa caaacagagc cgtcgtgttg ttcccaggga 300

gaaaaatatt tatgttcagt gatgcgagta tagggcacat ccacagaaca gtagttcatc 360

actgcgcac cctgg 375

<210> 54

<211> 400

<212> DNA

<213> Klebsiella sp.

<400> 54

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acaatccgct agcgagtatg attcttagtt ggcgtagattt attcatgaat gggactctta 120

attttgagta tattttctata ctctattttta cgggaattat tttgacgggt gtcggtttgt 180

ctattttcaa taaattaa tctcgatttg cagagatcta aaagtgcgct ataagagcag 240

catgctaggc tatttatggt cagtagcaaa tccattgctt tttgccatga tttactattt 300

tatatattaag ctggtaatga gagtacaaat tccaaattat acagttttcc tcattaccgg 360

cttgtttccg tggcaatggt ttgccagttc ggccactaac 400

<210> 55

<211> 413

<212> DNA

<213> Klebsiella sp.

<400> 55

cgagccaccc actgtagcgt atggatatcg cgcaagccgc cggggctgct tttcacgtcc 60

ggctcgaggt tatagctggt gccatgatag cgctgatgac ggacgttctg ctcttcgacc 120

ttggcgcgga agaacttttc cgatggccag aagccgtcgc taaaaatatg tttttgcagt 180

tcaaggaaca gcgcgacgtc gccgatcagc aggcgcgatt cgattaagtt ggtggcaacg 240

gtcagatccg agagaccttc cagcaggcac ttttcgaggg tgcgtacgct gtggcccacc 300

tccagcttga cgtcccacag cagggtgagc agttcgccga ctttttgcg cgtgtcgtcc 360

09743PC.ST25.txt

ggcagttttt tacgactgag gatcagcaga tcgacgtctg agagcgggtg cag 413

<210> 56
<211> 500
<212> DNA
<213> Klebsiella sp.

<400> 56
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ccggtgctgg aagagatgcg cgcaaagggg atgaacctca gcggtccgct gccggcagac 120
actctctttc agccgaaata tcttgatcat gccgatgcgg tactcgcgat gtaccacgat 180
cagggcctgc ccggtgctaaa ataccagggc tttggccgcg gcgtgaacat tacgctcggg 240
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aaagcggacg tcggcagttt tatcacggcg cttaatctcg ccatcaaaat gattgttaat 360
accaatgaa taatcgagtc catcagggcc atttagcccg caaacgcttc gggcagaact 420
tcctcaacga tcagtttctg atcgacagca tcgtctcggc gattaaccg cagaaaggcc 480
aggcgatggt tgaaatcggc 500

<210> 57
<211> 473
<212> DNA
<213> Klebsiella sp.

<400> 57
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ggaagaagtt tgcgcacgtc agatcgacgc cgtgctgaaa acccagggcg ctgccgcttt 120
cgaaggcgtg gttatcgctt acgaaccagt atgggctatc ggtaccggca aatcagcgac 180
cccggctcag gcgcagggcg tgcacaaatt catccgtgac cacattgcta aagctgacgc 240
caaaatcgct gagcaagtga tcatccagta cggcgggttc gttaacgctg gcaacgccgc 300
agagctgttc acccagccgg acatcgacgg cgcgctggtt ggcggcgcct cctgaaagc 360
tgacgctttc gcggtgatcg ttaaagcagc agaagcagcg aaaaaagcgt aattcgcttt 420
tcccggtggc gacacgcgac cgggttgact gacaaaacgt gggagcccgg cct 473

<210> 58
<211> 463
<212> DNA
<213> Klebsiella sp.

<400> 58
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taatttttgt gtacgctctg acgagcgcac aataaaacaa gacgaatttt tgaacaattg 120
tctttaaatt tggttaattga attgatctgt tggtgtttta aggtatttga atttcttttg 180

09743PC.ST25.txt

tatagatatg taaattaaca ttgaaaagcc atttcaaaaa ttaaataatat ggcgaacata 240
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 tatttcgcac atcaaaataa ctcttttttc ttctgtttgt tattcatggc catctattgg 360
 cgaaataagg cagagtagag ggggatgtgc ctaatatcct gcggaaggaa cgcaatgtac 420
 atttacaggg aggagctgac gagccgtttc gcgatagctt tag 463

<210> 59
 <211> 526
 <212> DNA
 <213> Klebsiella sp.

<400> 59
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 gaagagtatt ttcttctgac agcatgcctt taaaattatt gcggcagttt actattgctg 120
 catataaata tattgccagt aataagcgct gtatatattat gtttgaacat gaccgcgaca 180
 gaaaaaaact ggctaagttg gttggactcg aagaacaaca gactattggt attgatgggtg 240
 caggcattaa tccagagata tacaatatatt ctcttgaaca ggatcacgat gtccctgttg 300
 tattgtttgc cagccgtatg ttgtggagta aaggactggg cgacttaatt gaagcgaaga 360
 aaatattacg cagtaagaat attcacttta ctttgaatgt tgctggaatt ctggtcgaaa 420
 atgataaaga tgcaatttcc cttcagggtc attgaaaatt ggcacagca aggattaatt 480
 aactggttag gtcgttcgaa taatgtttgc gatcttattg agcaat 526

<210> 60
 <211> 473
 <212> DNA
 <213> Klebsiella sp.

<400> 60
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 gattgctgaa cgtaagatca agttcctgct gcgcgccag gcgcaggtgc aggtggtcgc 120
 tgaaacgctg tcaccggcgc tggccgatct ggctgcgcgc caggcactca gctggcgggc 180
 gacggcattc agcgactcgc tgggtggatga tgtctttctg gtgattgcgg ccaccgagga 240
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 ggtggataac caggcgctgt gtcggtttgt tttcccttct atcgtcgacc gttcgccgct 360
 gctgggtggc atctcctcca gcggtaaagc gccggtgttg tcgcgcattc tgcgtgaaaa 420
 aatcgaagcg ctgctgccga cgaatctcgg tcggctggcg gaatcagcaa gct 473

<210> 61
 <211> 451
 <212> DNA
 <213> Klebsiella sp.

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<400> 61

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gcaaatgcta aaaaaggag aggggattac cagctggcgg gcttttccgc gccgagatta      180
tccagcacgg cgcgcgagcg caggccgtca ggaaagtgaa ggtccggggc gatctcgaac      240
agcggccaga gcataaagcc gcggtttttc atatcgtagt gcggaacggg caggcgctcg      300
ctgttaatga cagcatcgcc aaacagcatg atatcgaggt ccagcgtgcg cggccccag      360
cgttcgggctt tgcgcactcg cccctgctgc agttcgatgc gctgagtatg atcgagcagc      420
gtctcggggg gcagggcggt ttccagcgca a                                          451

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<210> 62

<211> 525

<212> DNA

<213> *Klebsiella* sp.

<400> 62

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ggcttaacgc cagctatgtc aacgotgcgg ttatgcggat ttttcatgcc tctgcggcta      60
acagaaaaaa gccttatgat agctatacta atggggcttt ttactccgtt ttgaccgat      120
tcctgaccgg cgtcagggtc aagtcacaaa aatcatcaca attttccgtc accggcgcta      180
caatcgaccg aagtcacaat ctcaaatacag aagagtattg ctaatgaaaa acatcaaccc      240
aacgcagacc tctgcctggc aggcattaca gaaacacttc gacgaaatga aagatgtcac      300
tatcagcgag cttttcgcca aagatagcga ccgtttttct aaattttccg cgacgttcga      360
cgatctgatg ctgggtggact tctccaaaaa ccgcactact gaagagacgc tggctaaact      420
gcaggatctg gcgaaagaga ctgacctggc gggcgctatc aagtcgatgt tctcagggtga      480
gaagatcaac cgcaccgaag accgcgcggt actgcacgtc gcgct                          525

```

<210> 63

<211> 475

<212> DNA

<213> *Klebsiella* sp.

<400> 63

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tgcttcatcc gcatttcctt gaaatattatt tgggtcttagg cggacggtag agcgctaata      60
gctcgtccac ctttttacgc gtaccaccgt tgctgctgat gctgcgccgc accttcacaa      120
tatgcgtttc tgccgcgttt ttataaccatt cctgcgtcag cggcgtgcgg tggttgaaa      180
tcagcaccgg gatgcgcttt ttcatacagc attccgcctt ttgcgccagc agtacctgtt      240
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catagggcgg atcgcaatac accactgtgc ggctatccgc acgttgcatg cactcttcgt      360
aagattcgca gtaaaactcg gcgttttgcg ctttctcggc gaaatgatag agctcagctt      420
cggggaaata gggcttttta taacggccaa acggcacatt gaactcgccg cgcag          475

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<210> 64
<211> 286
<212> DNA
<213> *Klebsiella* sp.

<400> 64
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cctgcgataa cagcgattca aaagcgccaa ccgttggcgc agcagcggag agcaatgcca 120
gcggccaggc aatcagcctg ctggatggca agctgagctt caccctgcct gcgggcatgg 180
ccgaccagag cggcaaactg ggtaccagg cgaacaatat gcacgtctac tctgacgcta 240
ccggccagaa agcgggtcatc gtcacgtcg gcgacagcac caatga 286